

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 17:46:27 ; Search time 7009 Seconds  
(without alignments)  
11441.487 Million cell updates/sec

Title: US-10-607-752-115  
Perfect score: 1655  
Sequence: 1 gatctatctactcgaccttc.....atccaccatcaccatcactga 1655

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 4708233 seqs, 24227607955 residues 9416466  
Total number of hits satisfying chosen parameters:

imum DB seq length: 0  
imum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pt:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1655	100.0	1749	6 AR201278	Sequence
2	1011.4	61.1	1749	6 AR201276	Sequence
3	740.2	44.7	1749	6 AR201277	Sequence
4	291	17.6	291	6 AR201235	Sequence
5	261	15.8	261	6 AR201238	Sequence
6	226	13.7	697	6 AR201234	Sequence
7	210	12.7	210	6 AR201233	Sequence
8	177	10.7	177	6 AR201241	Sequence
9	147	8.9	147	6 AR201236	Sequence
10	138	8.3	138	6 AR201237	Sequence
c 11	132.4	8.0	299925	1 AP005039	Streptomy
12	132	8.0	132	6 AR201240	Sequence
13	126.6	7.6	309050	1 SC0939117	Streptomy
14	114	6.9	114	6 AR201231	Sequence
c 15	102.4	6.2	110000	1 AP006618_17	Continuation (18 o
16	101.6	6.1	300684	1 AE017227	AE017227 Mycobacte
17	96	5.8	96	6 AR201229	Sequence
c 18	95.6	5.8	1245	6 AR389420	Sequence
19	95.6	5.8	1371	6 AR389265	Sequence

c 20	88.8	5.4	3712	1 AB117722	AB117722 Rhodococc
c 21	86	5.2	277000	1 SC0939109	AL939109 Streptomy
c 22	80.6	4.9	300330	1 AP005222	AP005222 Corynebac
23	79.2	4.8	110000	1 AP006618_36	Continuation (37 o
24	78	4.7	298550	1 AP005047	AP005047 Streptomy
25	77.6	4.7	110000	1 AP006618_24	Continuation (25 o
c 26	77.6	4.7	186752	9 AC111200	AC111200 Homo sapi
c 27	76.2	4.6	125020	9 AF429315	AF429315 Homo sapi
c 28	75	4.5	75	6 AR201230	AR201230 Sequence
c 29	74.2	4.5	213050	1 AL646067	AL646067 Ralstonia
c 30	71	4.3	1393	11 PM11H12G	AL684264 Penicilli
c 31	70.2	4.2	349640	1 BX572600	BX572600 Rhodopseu
c 32	69.8	4.2	28890	1 AF512431	AF512431 Saccharot
c 33	69.2	4.2	4725	6 AX697993	AX697993 Sequence
c 34	69.2	4.2	11092	1 AE005703	AE005703 Caulobact
c 35	69.2	4.2	60196	6 AX697977	AX697977 Sequence
36	68.8	4.2	1393	11 PM11H12G	AL684264 Penicilli
37	68.4	4.1	1314	6 BD164882	BD164882 Novel pol
38	68.4	4.1	1314	6 AX122785	AX122785 Sequence
39	68.4	4.1	1330	6 AX063723	AX063723 Sequence
40	68.4	4.1	1330	6 AX064023	AX064023 Sequence
41	68.4	4.1	1330	6 AX064049	AX064049 Sequence
42	68.4	4.1	1330	6 AX064237	AX064237 Sequence
43	68.4	4.1	1330	6 AX244019	AX244019 Sequence
44	68.4	4.1	1371	1 AY238324	AY238324 Corynebac
45	68.4	4.1	1491	6 AX063721	AX063721 Sequence

ALIGNMENTS

RESULT 1  
AR201278 LOCUS 1749 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 58 from patent US 6358734.  
ACCESSION AR201278  
VERSION AR201278.1 GI:20252166  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 1749)  
AUTHORS  
TITLE  
Compounds for treatment of infectious and immune system disorders  
and methods for their use  
JOURNAL  
Patent: US 6358734-A 58 19-MAR-2002;  
FEATURES  
Location/Qualifiers  
source  
1. 1749  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match	100.0%;	Score	1655;	DB	6;	Length	1749;
Best Local Similarity	100.0%;	Pred. No.	1.1e-211;	Indels	0;	Gaps	0;
Matches	1655;	Conservative	0;	Mismatches	0;		
Qy	1	GATCTATCTACTCGACCTTCGCGACCGCGGTGACCGGGTGGCTTCTGACGTTACTCGGCC	60				
Db	95	GATCTATCTACTCGACCTTCGCGACCGCGGTGACCGGGTGGCTTCTGACGTTACTCGGCC	154				
Qy	61	ATCCGCTGGCGACCGCTTCGCGCGGTTCGCGACGATCAACCGGATCGAAGAGCATGG	120				
Db	155	ATCCGCTGGCGACCGCTTCGCGCGGTTCGCGACGATCAACCGGATCGAAGAGCATGG	214				
Qy	121	TGGCCAAAGCTGCGCGCATCGCGAGGAGGTCTCGGACCGGGTCTCGCGCATCTCGCGC	180				
Db	215	TGGCCAAAGCTGCGCGCATCGCGAGGAGGTCTCGGACCGGGTCTCGCGCATCTCGCGC	274				
Qy	181	CCGGGACCGTTTGGTTCGGTTCGGGAACTCCGCGGCTTCGCGCTTCTTGGGCGGGATCTGATC	240				
Db	275	CCGGGACCGTTTGGTTCGGTTCGGGAACTCCGCGGCTTCGCGCTTCTTGGGCGGGATCTGATC	334				
Qy	241	CAGAACGGGCGCGGTCTCGGGTTGAGGTTCTCGGTGCCCGCTCGCGCTCGACGCGACGTCG	300				

Db 335 CAGAACGGGCGGCTCTCGGCGTTGAGGTTCTCGGTGCCAGTGCCTCGACGCGCATGTCG 394  
Qy 301 TCGGCGCTGTGATGAGCGCGCGCTGAGGCTCTCGGTCCAAACGTCAAGACCGGTGCC 360  
Db 395 TCGGCGCTGTGATGAGCGCGCGCTGAGGCTCTCGGTCCAAACGTCAAGACCGGTGCC 454  
Qy 361 GGGCGGATGATCTATCAGTTTCGGGCTCGGTCCGACGCGCGCGGAGGCGAGCTTCGG 420  
Db 455 GGGCGGATGATCTATCAGTTTCGGGCTCGGTCCGACGCGCGCGGAGGCGAGCTTCGG 514  
Qy 421 CTCGGGCGTCCGATCGGGTTCGGTTCGGTCCGGCCAGACACACGATCCACCCGAGTCCA 480  
Db 515 CTCGGGCGTCCGATCGGGTTCGGTTCGGTCCGGCCAGACACACGATCCACCCGAGTCCA 574  
Qy 481 GCAACGGGTCCTCCGACGCTGCA CATCTCCAGTTCGATGAACGCGCGAGCTCGGGGACGT 540  
Db 575 GCAACGGGTCCTCCGACGCTGCA CATCTCCAGTTCGATGAACGCGCGAGCTCGGGGACGT 634  
Qy 541 CGCGGCGCAGCAGCAGCTGTTTCAGATGGCAGTTCGCGGTGCAATGCCGGTTCGGGCT 600  
Db 635 CGCGGCGCAGCAGCAGCTGTTTCAGATGGCAGTTCGCGGTGCAATGCCGGGTTTCGGGCT 694  
Qy 601 CGTTCGGGCTTCGCGAGTTCAGCAGTTCGGCGGAGCAGATGCACCGAGCGGAACGACTCGG 660  
Db 695 CGTTCGGGCTTCGCGAGTTCAGCAGTTCGGCGGAGCAGATGCACCGAGCGGAACGACTCGG 754  
Qy 661 GCGCGGATCTGATCAGCTCGGGAGCGGGTCCGACGAAACGCCAGCGTGGGAAACACC 720  
Db 755 GCGCGGATCTGATCAGCTCGGGAGCGGGTCCGACGAAACGCCAGCGTGGGAAACACC 814  
Qy 721 GAGACGGGCGGATGTCGCGCGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780  
Db 815 GAGACGGGCGGATGTCGCGCGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 874  
Qy 781 CCGCGGACCGCTCGGAGTGCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840  
Db 875 CCGCGGACCGCTCGGAGTGCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 934  
Qy 841 CACGGGATGATCTGATTCGCGAGGATCACGAAACAGTAAAGCGGTTCGCGTTGAATCCA 900  
Db 935 CACGGGATGATCTGATTCGCGAGGATCACGAAACAGTAAAGCGGTTCGCGTTGAATCCA 994  
Qy 901 ATGTGCTGTGACGAGGATCGATGCGGACACGAGCAGCGGAGTCCGATCTGTC 960  
Db 995 ATGTGCTGTGACGAGGATCGATGCGGACACGAGCAGCGGAGTCCGATCTGTC 1054  
Qy 961 TCGCGACCTTCGCGGTTCACGCGCGGTTCGTCGTCGCGAAACCGCGCGCGATGTCGCGCG 1020  
Db 1055 TCGCGACCTTCGCGGTTCACGCGCGGTTCGTCGTCGCGAAACCGCGCGCGATGTCGCGCG 1114  
Qy 1021 CCGGTGCGGCGGTCTTCATGCGCGGTTCGTTTCAGTTCGTCGTCGCGGTGCTGTTCTGC 1080  
Db 1115 CCGGTGCGGCGGTCTTCATGCGCGGTTCGTTTCAGTTCGTCGTCGCGGTGCTGTTCTGC 1174  
Qy 1081 GAAAGGCG 1140  
Db 1175 GAAAGGCG 1234  
Qy 1141 CAGCGGTACTTTCG 1200  
Db 1235 CAGCGGTACTTTCG 1294  
Qy 1201 GCCAGATACACCGAGCGGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260  
Db 1295 GCCAGATACACCGAGCGGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1354  
Qy 1261 TGGAGATCGGATCTTATCGCGCGGTTCGCGGAGGAGCGCGGTAGCGCGGTTCGACT 1320  
Db 1355 TGGAGATCGGATCTTATCGCGCGGTTCGCGGAGGAGCGCGGTAGCGCGGTTCGACT 1414  
Qy 1321 ACSTGCGCGCGGTTCGCGGAGAGCAGGACTACATCGACCGAGCGCTTCGCGCAACATCGGCG 1380

Db 1415 ACGTCGCGCGGTTCGCGGAGAGCAGGACTACATCGACCGAGCTTCGCGCAACATCGGCG 1474  
Qy 1381 CGTATCTGCCAGCTGAGGTTCCGCTCTCGTTCGATCTATCGCGCGCAACCGCGCGGTGC 1440  
Db 1475 CGTATCTGCCAGCTGAGGTTCCGCTCTCGTTCGATCTATCGCGCGCAACCGCGCGGTGC 1534  
Qy 1441 CCGGCAACCGCGTGGATCGTTTCGTAGTACCCGGAAGCTCTTGAGAGCTAAGGCCAATTGGG 1500  
Db 1535 CCGGCAACCGCGTGGATCGTTTCGTAGTACCCGGAAGCTCTTGAGAGCTAAGGCCAATTGGG 1594  
Qy 1501 AAGATATCTGGACCTTCCCATCAATAGAGGAAAGATCGCCCTAGGGGATCCGTAGCGG 1560  
Db 1595 AAGATATCTGGACCTTCCCATCAATAGAGGAAAGATCGCCCTAGGGGATCCGTAGCGG 1654  
Qy 1561 GCCCGGTGTTTCAGTGAACCTTGGGCGGCGGCAATCCCATCGCGCGCAACCGCGGAGCGG 1620  
Db 1655 GCCCGGTGTTTCAGTGAACCTTGGGCGGCGGCAATCCCATCGCGCGCAACCGCGGAGCGG 1714  
Qy 1621 AAATCCACGATCCCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1655  
Db 1715 AAATCCACGATCCCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1749

RESULT 2  
AR201276  
LOCUS AR201276 1749 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 56 from patent US 6358734.  
ACCESSION AR201276  
VERSION AR201276.1 GI:20252164  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1749)  
AUTHORS Delcayre,A.  
TITLE Compounds for treatment of infectious and immune system disorders  
and methods for their use  
JOURNAL Patent: US 6358734-A 56 19-MAR-2002;  
FEATURES  
source  
1..1749  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 61.1%; Score 1011.4; DB 6; Length 1749;  
Best Local Similarity 78.9%; Pred. No. 7.9e-126;  
Matches 1329; Conservative 0; Mismatches 296; Indels 60; Gaps 8;

Qy 1 GATCTATCTACTCGACCTTCGCGCGGCGGTACCCGGGTGGCTCTGACGTACTCCGGCC 60  
Db 95 GATCTATCTACTCGACCTTCGCGCGGCGGTACCCGGGTGGCTCTGACGTACTCCGGCC 154  
Qy 61 ATCCGCTGCGGACCGGCTGCGGCTCGGACGATCAACGCGATGGAAGACGAGGCGATGG 120  
Db 155 ATCCGCTGCGGACCGGCTGCGGCTCGGACGATCAACGCGATGGAAGACGAGGCGATGG 214  
Qy 121 TGGCCAAACGCTCCCGCATCGCGGAGCGAGTCTCGGACCGGCTCTGCGGATCTCGCGG 180  
Db 215 TGGCCAAACGCTCCCGCATCGCGGAGCGAGTCTCGGACCGGCTCTGCGGATCTCGCGG 274  
Qy 181 CCGGCGACCTTCGGTTCGGCGGAGTTCGCGGCTCTGCGGCGGATCTGATC 240  
Db 275 CCGGCGACCTTCGGTTCGGCGGAGTTCGCGGCTCTGCGGCGGATCTGATC 334  
Qy 241 CAGAACCGGCGCGGTCTCGGCGGTGAGGCTCTCGGTGCCAGTCCGCTCGACGCGAGTGG 300  
Db 335 CAGAACCGGCGCGGTCTCGGCGGTGAGGCTCTCGGTGCCAGTCCGCTCGACGCGAGTGG 394  
Qy 301 TCGGCGCTGCTGATCGGCGCGGTAGGCTCTCGGTCCCAACGTCAGACCGGTGCC 360  
Db 395 TCGGCGCTGCTGATCGGCGCGGTAGGCTCTCGGTCCCAACGTCAGACCGGTGCC 454  
Qy 361 GGGCGGATGGATCTATCAGTTTCGGGCTTCGTCGCGCGCGCGCGCGCGCGCGCGCGCG 420

Db 455 GGGCGGATGATCT---GATCGGACGGCATACGAAACAGTAAGCGGTTCGGTTGAA 510  
Qy 421 CTCCGGGTCGATCGGGTGGGTCCGTCCGGCCAGCACACAGCATCCACCCGAGTCCA 480  
Db 511 TCCAATGTGTGTCAGAGGATCCGA-----TGCCGAACACCGACACCGAGAGTTC 564  
Qy 481 GCAACGGGTCGCCGACGGTGCATCTCCAGTTCGATGAACCGCGGAGCTCGGGGACGT 540  
Db 565 GCATCTGTCTCGGACCTTGGGTCAAGGGGGTGTGGCTCCGCAACCGCGCGGAT 624  
Qy 541 CGCGGCGACGACGACGTTGTTTCAGATGGCAGTTCGCCGTGCATGATCCCGGGTTCGGCGT 600  
Db 625 GTCCGCGCGCGCT-----GCGGCGGCTCTCCATGGCGCGTTCGTTCACT 671  
Qy 601 CGTCGGGCTTCGCGGATCGAGCTCAGCGAGTCGCGGAGCACATGCACCGAGCGGAGCATCGG 660  
Db 672 CGTCGTCCGGTGGCTGTTCTCGGAACGGGCGCGCGCGCGCTGCTCCG-----TCCG 724  
Qy 661 GCGCGGATCTGATCAGTCCGGGAGCGGGTGCACGAAACCGCAGCGTGGGAGCACC 720  
Db 725 ATACGGGATCTGATCAGCTCGGGAGCGGGTGCACGAAACCGCAGCGTGGGAGCACC 784  
Qy 721 GAGACGGCGGATGTGCGCGCAGCAGCGCCAGCGGTGCACCCCGGGGACCGGGCC 780  
Db 785 GAGACGGCGGATGTGCGCGCAGCAGCGCCAGCGGTGCACCCCGGGGACCGGGCC 844  
Qy 781 CCGCGGACCGCGTGGAGTGCACCCCGCGCGCACCGCGCGCGCGTGTGCACATCAGC 840  
Db 845 CCGCGGACCGCGTGGAGTGCACCCCGCGCGCACCGCGCGCGCGTGTGCACATCAGC 904  
Qy 841 CAGCGGATGATCT---GATCGGACGAGTACGAAACAGTAAGCGGTTCGGTTGAA 896  
Db 905 CAGCGGATGATCTATCAGTTTCGGCTTGGTTCGCGACCGCGCGGAGCGAGTTCG 964  
Qy 897 TCCAAATGTGTGTCAGCAGGATCCGA-----TGCGGAACACCGACCAACCGGAGCAGTC 950  
Db 965 CTCGGGCGTGCATCGGGTGGTCCGTCCGCGCAGCACACAGCATCCACCGAGTCCA 1024  
Qy 951 GCAATCTGTCTCGGACCCCTGGGTGCACGGGCGTGTGGCTCGGCAACCGCGCGGGAT 1010  
Db 1025 GCAACGGTCCCGACCGTGCATCTCCAGTGCATGAACGCGCGGAGTCTCGGGACGT 1084  
Qy 1011 GTCCGCGCGCGCT-----GCGGCGGCTCTCCATGGCGGTTCGTTCACT 1057  
Db 1085 CGCGGCGACGACGACGTTGTCAGATGGCAGTCCCGTGCATGATCCCGGTTCCGCGT 1144  
Qy 1058 CGCTCGTCCGTGGCTGTCTCGAAACGGGCGCGCGCGCGCTGCTCCG-----TCCG 1110  
Db 1145 CGTCGGGCTTCGCGAGTCCAGCNGTTCGGGAGCACATGCACCGAGGACGACTCCG 1204  
Qy 1111 ATACGGGATCTATCAGCAGGTAGCGTCCAGCGTACTTTCGCGCCCAAGAACAGCGGT 1170  
Db 1205 GCGCGGATCTATCAGCAGGTAGCGTCCAGCGTACTTTCGCGCCCAAGAACAGCGGT 1264  
Qy 1171 GCGTCCGCGGACAGCGGTCTTCGCGCAGATACACCCAGGCGGTGGCGGCATG 1230  
Db 1265 GCGTCCGCGGACAGCGGTCTTCGCGCAGATACACCCAGGCGGTGGCGGCATG 1324  
Qy 1231 TCCAGATCTGTGGCAGCGCGCGGACGCGTGGAGATCGGATCTATCGCGCGGTGTCG 1290  
Db 1325 TCCAGATCTGTGGCAGCGCGCGGACGCGTGGAGATCGGATCTATCGCGCGGTGTCG 1384  
Qy 1291 GGAAGGACGAGCGCGTAGCGGCTTGCACTACGTCCCGCGGTGGCGAAGCAGGACT 1350  
Db 1385 GGAAGGACGAGCGCGTAGCGGCTTGCACTACGTCCCGCGGTGGCGAAGCAGGACT 1444  
Qy 1351 ACATCGACGAGCGCTTGGCGAACATCGGCGGATCTGCCAGCTGAGGTTCCCGCTTCG 1410  
Db 1445 ACATCGACGAGCGCTTGGCGAACATCGGCGGATCTGCCAGCTGAGGTTCCCGCTTCG 1504  
Qy 1411 TCGGATCTATCGCGCGCACCGCGCGGTGCGCGCACCGGTCGTTGATCGTTTCAGTACC 1470

Db 1505 TCGGATCTATCCCGCCACCGCGCGGTGCCCGCACCGGTGGATCGTTCTCAGTACC 1564  
Qy 1471 CGAAGCTCTTGAGAGCTAAGGCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGAGG 1530  
Db 1565 CGAAGCTCTTGAGAGCTAAGGCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGAGG 1624  
Qy 1531 AAAAGATCGCCCTAGGGATCCGTAGCGGGCCCGTGTTCGAGTGAACCTTGGGCGAGG 1590  
Db 1625 AAAAGATCGCCCTAGGGATCCGTAGCGGGCCCGTGTTCGAGTGAACCTTGGGCGAGG 1684  
Qy 1591 CAATCCCATCGCGCAGCGCCGCGAGCGGAAATCCACGATCCCATCACCATCACCATC 1650  
Db 1685 CAATCCCATCGCGCAGCGCCGCGAGCGGAAATCCACGATCCCATCACCATCACCATC 1744  
Qy 1651 ACTGA 1655  
Db 1745 ACTGA 1749

RESULT 3  
AR201277  
LOCUS AR201277 1749 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 57 from patent US 6358734.  
ACCESSION AR201277  
VERSION AR201277.1 GI:20252165  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1749)  
AUTHORS Delcayre,A.  
TITLE Compounds for treatment of infectious and immune system disorders  
and methods for their use  
JOURNAL Patent: US 6358734-A 57 19-MAR-2002;  
FEATURES Location/Qualifiers  
source  
1. .1749  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 44.7%; Score 740.2; DB 6; Length 1749;  
Best Local Similarity 69.0%; Pred. No. 1.2e-89;  
Matches 1244; Conservative 0; Mismatches 263; Indels 296; Gaps 5;

Qy 1 GATCTATCTACTCGACCTTTCGCGACCGCGGTACCCCGGTGGCTGACGTACTTCGGGCC 60  
Db 95 GATCTATCTACTCGACCTTTCGCGACCGCGGTACCCCGGTGGCTGACGTACTTCGGGCC 154  
Qy 61 ATCCGCTGGCGACCGCTTCGCGGTTCGCGACGATCAACGCGATGGAAGACGAAGGATGG 120  
Db 155 ATCCGCTGGCGACCGCTTCGCGGTTCGCGACGATCAACGCGATGGAAGACGAAGGATGG 214  
Qy 121 TGCCCAACGCTGCCCGATTCGCGGAGCAGGTGCTCGGACCGGGTCTGCGCGATCTCGCG 180  
Db 215 TGCCCAACGCTGCCCGATTCGCGGAGCAGGTGCTCGGACCGGGTCTGCGCGATCTCGCG 274  
Qy 181 CCGCGCACCGTTCGCTCGCGAAGTCCCGGCTTCGCGCTTCCTGCGCGGATCTGATC 240  
Db 275 CCGCGCACCGTTCGCTCGCGAAGTCCCGGCTTCGCGCTTCCTGCGCGGATCTGATC 324  
Qy 241 CAGAACGGGCGGCTCTCGGGTTGAGGTCTCTCGGTGCCAGTGCCTGCGACGCGACGTG 300  
Db 325 ----- 324  
Qy 301 TCGGCGCTGATGATGCGGCGCGCGGTGCGGTCTCTCGGTCCACACGTCAGCAGCGTCCG 360  
Db 325 ----- 324  
Qy 361 GGGCGGATGATCTATCAGTTTCGGCCCTGCTGCGCAGCCCGCGGAGGCGAGCAGTTCCG 420  
Db 325 -----GGATCTATCAGTTTCGGCCCTGCTGCGCAGCCCGCGGAGGCGAGCAGTTCCG 376  
Qy 421 CTCGGGCTGATCGGGTTGGGTTCGCTCGGCGCAGCACACGAGCATCCACCGAGGTCCA 480

Db 377 CTCGGCGTCGATCGGGTTGGTCTCGCGCAGACACAGCATCCACCCGAGGTGCA 436  
 QY 481 GCAACGGGTCCTCCGACCGGTGCAATCTCCAGTCGATGAACCCCGAGCTCGGGAGCT 540  
 Db 437 GCAACGGGTCCTCCGACCGGTGCAATCTCCAGTCGATGAACCCCGAGCTCGGGAGCT 496  
 QY 541 CGCGGCGCAGCAGCAGTGTGTTGATGTCAGATGCGCGTCGATGATCCCGGGTTCCGGGT 600  
 Db 497 CGCGGCGCAGCAGCAGTGTGTTGATGTCAGATGCGCGTCGATGATCCCGGGTTCCGGGT 556  
 QY 601 CGTCGGGCTCGCGGAGTCCAGCAGTCGCGGAGCAGCATGCAACCGAGGGAACAGTCCGG 660  
 Db 557 CGTCGGGCTCGCGGAGTCCAGCAGTCGCGGAGCAGCATGCAACCGAGGGAACAGTCCGG 616  
 QY 661 GCGCGGATCTGATCAGCTCGGGAGCCGGGTGCCAGCAACCGCAGCGTGGGAAGCAC 720  
 Db 617 GCGCGGATCTGATC-----GGCAGGATCAGCAACAGTAAAGCGTGTTCGGGT 666  
 QY 721 GAGACGGCGGATGTCGCGGAGCAGCGGCGGAGCGGTCGACCCCGGGAACCGGCG 780  
 Db 667 GAATCCAAATGTGTCGACGAGCATCCGATGCGGAACACCGACCAACCGGAGCATCGCA 726  
 QY 781 CGCGGACCGCTCGAGTCGACCCCGGCGGCGCACCGCGCGCGTGTGTCAGCATCAGC 840  
 Db 727 ATCTGTCTCGGACCTGTGGGTACCGGGGTGCTGGCTCCGGAACCCCGCGCATGTC 786  
 QY 841 CACGGGATGATCTGATCGCGAGGC---ATCAAGAACAGTAAGCGGTGTTCCGGTTGAAT 897  
 Db 787 GCGCGCGCTGCGGCGGCTCTCATGCGCGGTTCTGATGCTGCTCGTCCGGTGGCT 846  
 QY 898 CCNATGTGTGTCAGCAGGATCCGATGCGGAACACCGGACCGAGCAGTCGCAATCT 957  
 Db 847 GTTCTCGAAACGCGGCGCGCGCTGCTCGTCCGATACCGGATCTGATCAGTCGCG 906  
 QY 958 GTCTCGGACCTGTGGGTCAAGCGGCTGTGGCTCCGCAACCGCGCGCATGTCCGCG 1017  
 Db 907 GAGCGGGTCCAGCAACCGCAGCTGGGAGCACCGGAGCGCGCATGTGCGCGCG 966  
 QY 1018 GCGCGCTCGGCGGCTCTCCATGCGCGGTTCTGATGCTGCTGCTGCGGTGCTTC 1077  
 Db 967 CAGCAGCGCCAGCGCTGCAACCGCGGAGCACCGGCGCGCGGAGTCGAGTCGAC 1026  
 QY 1078 TCGGAAGCGGCGCGCGCGC-----CGTCTGCTCGATACGAGGATCTACGCGAG 1130  
 Db 1027 CCGCGCGCGCACCGCGCGCGTGTGTCAGCATCAGCAGCGGATGATCTATCAGCGAG 1086  
 QY 1131 GTAGGCGCTCCAGCGTACTCTTTCGCCCCAGAACAGCGGTGCGCTCGCGCGCAGAC 1190  
 Db 1087 GTAGGCGCTCCAGCGGTACTCTTTCGCCCCAGAACAGCGGTGCGCTCGCGCGCAGAC 1146  
 QY 1191 CGGTCTCGCGCAGATACACCCAGCGGTGCGCGCATGTTCAGATCGTGGCCAGCGCG 1250  
 Db 1147 CGGTCTCGCGCAGATACACCCAGCGGTGCGCGCATGTTCAGATCGTGGCCAGCGCG 1206  
 QY 1251 CGCGGACCGGTGAGATCGGATCTATCGCGGCTGTGGGGAAGCAGGCGCGTAGCG 1310  
 Db 1207 CGCGGACCGGTGAGATCGGATCTATCGCGGCTGTGGGGAAGCAGGCGCGTAGCG 1266  
 QY 1311 CGGTCTGATCTGCGCGCGTGTGGGGAAGCAGGATCTATCGACCGAGCTTTCGCG 1370  
 Db 1267 CGGTGATCTGCGCGCGTGTGGGGAAGCAGGATCTATCGACCGAGCTTTCGCG 1326  
 QY 1371 AATCGCGGCGGATCTGCGAGCTGAGGTTTCGCTCTCTGTCG----- 1413  
 Db 1327 AATCGCGGCGGATCTGCGAGCTGAGGTTTCGCTCTCTGTCG----- 1386  
 QY 1414 ----- 1413  
 Db 1387 GCGGCTCTCGGGTTGAGGTTCTCGGTGCGCATGTCGCGTGCAGCGAGCTGTCGCGGCT 1446  
 QY 1414 ----- 1413

Db 1447 GGTGATCGCGCGCGTAGGCGTCTCTGGTCCACAAAGTCGACAGCCGTGCGCGCGGAT 1506  
 QY 1414 -GATCTATCGCGGCAACCGGCGCGTTCGCGGCAACCGGTCGATGCTTCGTCAGTACCG 1472  
 Db 1507 GATCTATCGCGGCAACCGGCGCGTTCGCGGCAACCGGTCGATGCTTCGTCAGTACCG 1566  
 QY 1473 AAGCTCTTGAAGAGCTAAGGCAATTGGGAAGATATCTTGGACCTTCCCATCAATAGAGAA 1532  
 Db 1567 AAGCTCTTGAAGAGCTAAGGCAATTGGGAAGATATCTTGGACCTTCCCATCAATAGAGAA 1626  
 QY 1533 AAGCATCCCTAGGGATCCGTAGCGGCGCGGTGTTTCAGTGAATCTTGGGCAAGGCA 1592  
 Db 1627 AAGCATCCCTAGGGATCCGTAGCGGCGCGGTGTTTCAGTGAATCTTGGGCAAGGCA 1686  
 QY 1593 ATCCCATCGCGGCAACCGGCGGCAAGATCCACGATCCCATCACCATCACCATCAC 1652  
 Db 1687 ATCCCATCGCGGCAACCGGCGGCAAGATCCACGATCCCATCACCATCACCATCAC 1746  
 QY 1653 TGA 1655  
 Db 1747 TGA 1749  
 RESULT 4  
 AR201235  
 LOCUS AR201235 291 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 15 from patent US 6358734.  
 ACCESSION AR201235  
 VERSION AR201235.1 GI:20252123  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 291)  
 AUTHORS Delcayre, A.  
 TITLE Compounds for treatment of infectious and immune system disorders  
 and methods for their use  
 JOURNAL Patent: US 6358734-A 15 19-MAR-2002;  
 FEATURES  
 source  
 1..291  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 ORIGIN  
 Query Match 17.6%; Score 291; DB 6; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-29; Mismatches 0; Indels 0; Gaps 0;  
 Matches 291; Conservative 0;  
 QY 375 ATCAGTTCGGGCTCGTCCGCGCAGCGCGCGGAGCGAGGTCGCTCCGCGTCGATC 434  
 Db 1 ATCAGTTCGGGCTCGTCCGCGCAGCGCGCGGAGCGAGGTCGCTCCGCGTCGATC 60  
 QY 435 GGGTTGGGTCGTCGCGCGCAGCACACCGAGCATCCACCGAGGTCGAGCAACCGGTCGCCG 494  
 Db 61 GGGTTGGGTCGTCGCGCGCAGCACACCGAGCATCCACCGAGGTCGAGCAACCGGTCGCCG 120  
 QY 495 ACCTGTCACATCTCCAGTCGATGAACCGCGAGCTCGGGGAGCTCGCGCGCGAGCAGC 554  
 Db 121 ACCTGTCACATCTCCAGTCGATGAACCGCGAGCTCGGGGAGCTCGCGCGCGAGCAGC 180  
 QY 555 ACCTGTTTTCAGATGGCAGTCGCGGTCATGATCCCGGTTTCGCGGTCGTCGCGGCTTCGCG 614  
 Db 181 ACCTGTTTTCAGATGGCAGTCGCGGTCATGATCCCGGTTTCGCGGTCGTCGCGGCTTCGCG 240  
 QY 615 GAGTTCAGCAGTCGCGGAGCAGATGACCGAGCGGAGCAGTCCGGGCGG 665  
 Db 241 GAGTTCAGCAGTCGCGGAGCAGATGACCGAGCGGAGCAGTCCGGGCGG 291  
 RESULT 5  
 AR201238  
 LOCUS AR201238 261 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 18 from patent US 6358734.



```
Query Match      10.7%; Score 177; DB 6; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 672 GATCAGCTGGGAGCGCGGTGCCCCAGCAACGCGTGGGAGCAGCAGACCGGCGC 731
    |||||
Db 1 GATCAGCTGGGAGCGCGGTGCCCCAGCAACGCGTGGGAGCAGCAGACCGGCGC 60
    |||||

QY 732 GATGTCGCCGCGCAGCAGCGCCAGCGTGCACCCCGCGGGAACCGGCGCCCGGACCGC 791
    |||||
Db 61 GATGTCGCCGCGCAGCAGCGCCAGCGTGCACCCCGCGGGAACCGGCGCCCGGACCGC 120
    |||||

QY 792 GTCGAGTGCACCCCGCGCGCACCGCGCGCGCGTGCAGTCAGCAGCAGCGGAT 848
    |||||
Db 121 GTCGAGTGCACCCCGCGCGCACCGCGCGCGCGTGCAGTCAGCAGCAGCGGAT 177
    |||||

RESULT 9
LOCUS AR201236 147 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 16 from patent US 6358734.
ACCESSION AR201236
VERSION AR201236.1 GI:20252124
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 147)
AUTHORS Delcayre,A.
TITLE Compounds for treatment of infectious and immune system disorders
JOURNAL Patent: US 6358734-A 16 19-MAR-2002;
FEATURES Location/Qualifiers
source 1. .147
/mol_type="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      8.9%; Score 147; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1122 ATACGAGTAGGCGGTCCAGCGGTACTCTTCCGCCAGAACAGCGGTGCCGTGCCCGC 1181
    |||||
1 ATACGAGTAGGCGGTCCAGCGGTACTCTTCCGCCAGAACAGCGGTGCCGTGCCCGC 60
    |||||

QY 1182 GCAGCAGCGGTCTCTCGCCGAGATACACCCAGCGGTGCCGCGCATGTCCAGATCGTG 1241
    |||||
61 GCAGCAGCGGTCTCTCGCCGAGATACACCCAGCGGTGCCGCGCATGTCCAGATCGTG 120
    |||||

QY 1242 GCCAGCGCGCGCACCGGTGGAGATC 1268
    |||||
Db 121 GCCAGCGCGCGCACCGGTGGAGATC 147
    |||||

RESULT 10
LOCUS AR201237 138 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 17 from patent US 6358734.
ACCESSION AR201237
VERSION AR201237.1 GI:20252125
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 138)
AUTHORS Delcayre,A.
TITLE Compounds for treatment of infectious and immune system disorders
JOURNAL Patent: US 6358734-A 17 19-MAR-2002;
FEATURES Location/Qualifiers
source 1. .138
/mol_type="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      8.3%; Score 138; DB 6; Length 138;
Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1275 ATCCGCGCGCTGTCGGGAAGAGCAGGCGGTAGCGGTTGTCACCTAGTCGCCCGCGTT 1334
    |||||
Db 1 ATCCGCGCGCTGTCGGGAAGAGCAGGCGGTAGCGGTTGTCACCTAGTCGCCCGCGTT 60
    |||||

QY 1335 GCGCAGAGCAGGAGCTACATCGACCGAGCCCTTGGCAACATCGGCGCCTATCTGCAGCT 1394
    |||||
61 GCGCAGAGCAGGAGCTACATCGACCGAGCCCTTGGCAACATCGGCGCCTATCTGCAGCT 120
    |||||

QY 1395 GAGGTTCCGCTCTCGTC 1412
    |||||
Db 121 GAGGTTCCGCTCTCGTC 138
    |||||

RESULT 11
LOCUS AP005039/c 29925 bp DNA linear BCT 10-MAY-2003
DEFINITION Streptomyces avermitilis genomic DNA, complete genome, section 19/30.
ACCESSION AP005039 BA000030
VERSION AP005039.1 GI:29608072
KEYWORDS
SOURCE
ORGANISM Streptomyces avermitilis MA-4680
REFERENCE 1
AUTHORS Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C., Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osone,T., Kikuchi,H., Shiba,T., Sakaki,Y. and Hattori,M.
TITLE Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
MEDLINE 21477403
PUBMED 11572948
REFERENCE 2
AUTHORS Ikeda,H., Ishikawa,J., Hanamoto,A., Shinose,M., Kikuchi,H., Shiba,T., Sakaki,Y., Hattori,M. and Omura,S.
TITLE Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis
JOURNAL Nat. Biotechnol. 21 (5), 526-531 (2003)
MEDLINE 22608306
PUBMED 12692562
REFERENCE 3 (bases 1 to 299925)
AUTHORS Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C., Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osone,T., Kushida,N., Director-General of Biotechnology Center, Shiba,T., Sakaki,Y. and Hattori,M.
TITLE Direct Submission
JOURNAL Submitted (29-MAR-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424)
COMMENT This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akibaru Hanamoto(*3), Chigusa Takahashi(*3), Mayumi Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi Osone(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7) and Satoshi Omura(*1,*3).
Final finishing process and all annotation were done by H. Ikeda and J. Ishikawa.
*1 Kitasato Institute for Life Sciences, Kitasato University
*2 National Institute of Infectious Diseases
*3 The Kitasato Institute
```

\*4 National Institute of Technology and Evaluation  
 \*5 School of Science, Kitasato University  
 \*6 Institute of Medical Science, University of Tokyo  
 \*7 RIKEN, Genomic Sciences Center  
 Following url is also available.  
 http://avermitilis.lis.kitasato-u.ac.jp.

# FEATURES

## source

1. 299925  
 /organism="Streptomyces avermitilis MA-4680"  
 /mol\_type="genomic DNA"  
 /strain="MA-4680"  
 /db\_xref="taxon:227882"  
 /notes="This strain is also named as strain: ATCC 31267,  
 NCIMB 12804 or NRRL 8165.-synonym: Streptomyces  
 avermectinius"  
 39. .788

## CDS

/notes="SAV4416"  
 /codon\_start=1  
 /transl\_table=11  
 /product="putative two-component system response  
 regulator"  
 /protein\_id="BAC72128.1"  
 /db\_xref="GI:29608073"  
 /translation="MDOPEFGAEAVERGAGAGARLVVDDPTVAEVVSGYLDRA  
 GYVYDRAEDGPTALARAAPWDLVLDLMLPGMDGLEVCRRMRGPGVPVIMLTARGD  
 EDRIILGLEADYVTKPSRELVLVESVLRTPTVAPPLHSLGLADLPARR  
 ATKDGEALTIREFDLAFLRPGRAFSEDLREVMGWDFGDLSTVTVHVRRLRG  
 KVEDPARPLTIOTVWGVGVRFGTTPRQEA"

## CDS

/notes="SAV4417"  
 /codon\_start=1  
 /transl\_table=11  
 /product="putative two-component system sensor kinase"  
 /protein\_id="BAC72129.1"  
 /db\_xref="GI:29608074"  
 /translation="MMDMLLIALFALGAAAGLCGVLVLRRLSLTVSLAVSVA  
 AVTLAGTLAVAMFELSAHDLTVTVTVVMAAVSLATALLGLGWVARSRELALA  
 ARSFGDGPAAADGPTARELDALARELAATSARLAESDRERALESSRELAVMISH  
 DLRTPLAGLMSALEGDAADPDRLYLRQIRTEVERKINDMVDGLFELSRIHAGTLAL  
 SPRIILYLDGALADGAPLELRVDRVPEVPEVDEGKEMSRVLGNLLIAL  
 RRTPADGTVAIAAERSPGVLSVTDCGGIPEEDLPFRVDTGWRGTHTPTPAGAGL  
 GLAIVGIVEAHQQAARVNIPEGCREVTLPARAQPP"  
 1998. 3140

## CDS

/notes="SAV4418"  
 /codon\_start=1  
 /transl\_table=11  
 /product="hypothetical protein"  
 /protein\_id="BAC72130.1"  
 /db\_xref="GI:29608075"  
 /translation="MPGTVLLAASPAGKGLVDAAASVLPVLAAPSVLSGTDANV  
 VELADPLEQAVLTRLAATAAFGLTVFLAGLQQLORRORHLEPHILALARTPTSTVRYT  
 GFPHWTRBELRLPPGTTTLFVDLHADAEYTHLRTGLPDAGRAALYGRVAPPPR  
 RTVAPYAKAVATILRSRHPPEVLHEQALGRVAHEGGADI VLTTPGGGAALFPG  
 FVCPGAPYPPROPRTPDGPAADVHATIAAAGRAGHDAALAAQETAASTHGA  
 ASEALHWRERADLAMEAGDAFSCFAMLTAVGTRIAAGCAPADPAVEAAVRAHHQ  
 WGRIDDPARARELGPALADRLRVPGRREGALDHVQHLRLQLTQG"  
 complement (3180. .5276)  
 /note="SAV4419  
 similar to cell wall surface anchor family protein"

## CDS

/codon\_start=1  
 /transl\_table=11  
 /product="hypothetical protein"  
 /protein\_id="BAC72131.1"  
 /db\_xref="GI:29608076"  
 /translation="MKDLMRGHDDLHTRADGPPYLFRAWGFEIIVIRTLPTATAL  
 AVLPSSAALAVGSAADSLTLLPVRSTGDVVVDGQHORVFISSDPAGKVAWDTVA  
 GTVLGTVDSLPGARGLSADSGTLAAVPGADAI VADTATATEARYTGP  
 YPALAGDKIMFGYGGSEGNIGSLDLSGADPVVTLKQDTRTWDARILSSAGAPCT  
 LVAGAPGQSPVGLGVVSSGATLTAAHAPDVTGNGNLSDLVATPDGKDVVTASGA  
 PYQAVTKISDLSADGRQYNTYNAVDIAPDGTVAAGTFSWYDPDVHVPKPGVSTPV  
 ROYDLPTNGTSLDAGTLAGSLAWSPDGSRLLFVSYNDKDVYSLRVDPDPTKADTSLT  
 MVAPKATRGKLSVSGTLTSAEALPAGATVSVTRTDMESP SGKPGVGTATVAADGSYT  
 FGDTPPAGGKVTYATTAGDASHGATATGSVEVSRSTPTILTLLNDDKGVAYGSDVKF

TAHLGTTYKNRAVELWADPYGSKDKFKLVKSGTQVADGNLSVTLDLDRTKVTKAPAG  
 DARYAPKTAASAGAKVSVTSLSGFKYTKSAMGHTSYFHKSKDPVVTWTTWTPVNR  
 KOKLTVQAYNGAMHETASEYFALSAGSKSVTLGRTGTGIRFLRSAYINNSSGN  
 VNSTYGSWKYLIFTS"

## CDS

complement (5354. .5509)  
 /note="SAV4420"  
 /codon\_start=1  
 /transl\_table=11  
 /product="hypothetical protein"  
 /protein\_id="BAC72132.1"  
 /db\_xref="GI:29608077"  
 /translation="MFRRTAARYSRSAANAATVAALVAANAGPAPAAATPPAHEASH  
 SRLAPTP"

## CDS

5664. .7007  
 /note="SAV4421"  
 /codon\_start=1  
 /transl\_table=11  
 /product="putative regulatory protein"  
 /protein\_id="BAC72133.1"  
 /db\_xref="GI:29608078"  
 /translation="MADRDEPEIIIGRRVORLRAERGLTORQLAEPAATPAYISTLBAG  
 RYRASEPALRHIAIDRLGVAYEELATGRPAHLATLRLTLDAQRTLATGEAAEASQY  
 AALLAEAVHGLAAEBAALLGLGECATEAGDILVGRRRFEAEQRLGAPLRLVPA  
 ITRGAVSHYLAGELRVAVYLSTLDELNRTGLDHPDALLLLIYASVGYMDGMAAR  
 AAQAAEFALALAPQVGDPAALVARMHSVARTMLAEGRAAEDASLVKAELADVLHRRG  
 TELANWNRGYLHAQNGELERAEGLERQAHSMLAQRAALYSQAAVELADVLHRRG  
 KSDEAAALLHVLGDLSPERGAVHSAGAHRLIGIJAEDAHDTAAEAHEVYRALSLER  
 AGAAGDLADLCMLGDLLRSRGRVEALDAVRTGLHRTAGCTTTLGPAPAQPPL"

## CDS

complement (7322. .7543)  
 /note="SAV4422"  
 /codon\_start=1  
 /transl\_table=11  
 /product="hypothetical protein"  
 /protein\_id="BAC72134.1"  
 /db\_xref="GI:29608079"  
 /translation="MTKPSAPRRHLPSTPFAAPVAPAEAKHFGLDVRVSHDQFGLGTIV  
 GVEEGTAMLVDFGSGQARILPTTRMHSL"

## gene

complement (7614. .9236)  
 /genes="pbp7"

## CDS

complement (7614. .9236)  
 /genes="pbp7"  
 /notes="SAV4423"  
 /codon\_start=1  
 /transl\_table=11  
 /product="putative penicillin-binding protein"  
 /protein\_id="BAC72135.1"  
 /db\_xref="GI:29608080"

/translation="MSAPEEQRRRI PRVTRRRRRRWRIRRALAVALIMLCGA  
 VVAYLLTGVPHPETVSQSTVFLDAGEYLGRRGPDVDRQDVPVLRVPRVQDAVIA  
 AENRSPRTSGISPSAVVRAAVSTLGGARQGGSTITQYVKNALLSPEQSLSRKARE  
 ALIAVKLDTRSKDSILEGLVNTVYFGRGAAGIESAARNYFGVDAKDOLTUAQGAALAA  
 IINLPSYERAGADAKVTATLEKNSWLDGWRSTCTITAKERLAAAFPAFRVPPGN  
 TGRQYLLDAATEARDRLGTADQLAGRGYTVRTFDLAQAQATAEQVRGAPARK  
 GTRLHVALVPGDGAARVLYGGADYQPFNDVNGAVEAGTADDPFRAVFTGPL  
 AMLSRTPASPLRLASAAATVAGGTAKPTVYVAKITRGRTSYTARPDPTRRVVASVO  
 AOMLTKYGAAGAVGHFGSGSGPGARTLMOTTSGRLSVTVLFAEYPAAGKRPAR  
 PAHLPTAPVLAAGLTESVSKTLEVPAGLP"

## CDS

complement (9233. .9907)  
 /note="SAV4424"  
 /codon\_start=1  
 /transl\_table=11  
 /product="hypothetical protein"  
 /protein\_id="BAC72136.1"  
 /db\_xref="GI:29608081"  
 /translation="MSRTVPPPHAELEAREFARMADDVMSVPVLAIEIREGBARRR  
 RRTTALVTGCLLVLAFLAVYWRLLTPTADGATAPASVSGKAVRVVAAGERVQPLPG  
 AEIWLADGDEHMTAGSGVSLPEESRGAGPVTLRLEEVHDFLLSLGTYRGTOAA  
 ARVETPSGTACTLLTLAGSPGWSVYAIAPKPSAGKRLFATVRVTWYDARGAVLA  
 RSDGS"

## gene

complement (9904. .10341)  
 /genes="sig38"  
 complement (9904. .10341)  
 /genes="sig38"

/note="SAV4425"		VERSION	AL079353	AL096822	AL159178	AL355919	AL392189	AL442629	AL645882
/codon_start=1		KEYWORDS	Streptomyces coelicolor A3(2)						AL939117.1
/transl_table=11		SOURCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.						GI:24427162
/product="putative RNA polymerase ECF-subfamily sigma		ORGANISM	Streptomyces coelicolor A3(2)						
Query Match		REFERENCE	Bentley, S.D., Chater, K.F., Cerdeno-Tarraga, A.M., Challis, G.L., Thomson, N.R., James, K.D., Harris, D.E., Quail, M.A., Kieser, H., Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M., Cronin, A., Fraser, A., Goble, A., Hidalgo, J., Hornsby, T., Howarth, S., Huang, C.H., Kleser, T., Larke, L., Murphy, L., Oliver, K., O'Neill, S., Rabinowitch, E., Rajandream, M.A., Rutherford, K., Rutter, S., Seeger, K., Saunders, D., Sharp, S., Squares, R., Taylor, K., Warren, T., Wietzorrek, A., Woodward, J., Barrall, B.G., Parkhill, J., and Hopwood, D.A.						1
Best Local Similarity		AUTHORS	Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)						
Matches 202; Conservative 0; Mismatches 96; Indels 2; Gaps 1;		TITLE	Nature 417 (6885), 141-147 (2002)						
Qy 6 ATCTACTGACCTTCGCGGACCGGGCTACCCGGTGGCTGACGTACTCCGGCCATCCG 65		JOURNAL	Nature 417 (6885), 141-147 (2002)						
Db 158942 ATCGCGAGACCTTCGGGAAGCGGGCTTACCCGGCGGTCTGACCTACTCCGGGATCCG 158883		MEDLINE	21956410						
Qy 66 CTGGCGACCGCTCGCGGTGCGGACGATCAACGCGATGAGACCAAGGCATGTGGCC 125		PUBMED	12000953						
Db 158882 CTGCGCTGCGCGCCCGCGTGCACGATCAACGTCATGCGCGAGAGGGGTGCTCGAG 158823		REFERENCE	2 (bases 1 to 309050)						
Qy 126 AACGCTGCCCGCATCGCGAGCAGGTGCTCGGACCGGGTCTGCGCATCTCGCGCGCCCG 185		AUTHORS	Bentley, S.D.						
Db 158822 AACCGCGGAACCTCGCGCCCGGGTTCATCGAGCCGGGGTGGCGAGCTGGCCGAGCGG 158763		TITLE	Direct Submission						
Qy 186 CACCGTTGGTTCGGGAGAGTCCGGGCTCGGGCTCTTCTGGGCG--GGATCTGATCCAG 243		JOURNAL	Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces sequencing team, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: sdb@anger.ac.uk						
Db 158762 CACCGTCCGTGGCGAGGTGCGCGGTGTGCGCATGTTCTGGCGGCTGGAGCTGGTCAAG 158703		COMMENT	On or before Oct 30, 2002 this sequence version replaced gi:4725998, gi:4753846, gi:5019320, gi:5123864, gi:5139620, gi:5457234, gi:7210989, gi:7801279, gi:10178898, gi:10432457.						
Qy 244 AACGGCCGCTCGCGGTTGAGTCTCGTGCCTGCCAGTCCGTCGACGCGAGCTGCTCG 303		FEATURES	Location/Qualifiers						
Db 158702 GACCGGAGACGCGGAGCGCGTGTGTGCCGTACACCGCGCGGCGAGCGACGCGCCG 158643		Source	1..309050						
RESULT 12		Source	/organism="Streptomyces coelicolor A3(2)"						
AR201240		mol_type	genomic DNA						
LOCUS		strain	"A3(2)"						
DEFINITION		complement	(204..602)						
ACCESSION		note	"synonym: SCH5.07c"						
AR201240.1		complement	(204..602)						
VERSION		gene	SCH5.07c						
AR201240.1		CDS	SCH5.07c						
KEYWORDS		note	"SCH5.07c, putative membrane protein, len: 132 aa. Contains possible hydrophobic membrane spanning regions"						
SOURCE		codon_start	1						
ORGANISM		transl_table	11						
Unknown.		product	"putative membrane protein"						
Unclassified.		protein_id	"CAB38481.1"						
1 (bases 1 to 132)		db_xref	"GI:4539562"						
Delcayre, A.		db_xref	"UniProt/TREMBL:Q9X910"						
Compounds for treatment of infectious and immune system disorders		translation	"MGARTHPFSPVRPRRPHVYGRPRATAPGSGVSGSPFTSGSPA						
Patent: US 6358734-A 20 19-MAR-2002;		REPCVTASRLDTRGLEKRGCTGCTMESGPAIFAGVVFALFGALLVMTTRVRHGRPVA							
Location/Qualifiers		LCVSPVASATVASVAVALGLGAWCLTQV"							
1..132		complement	(622..2139)						
/organism="unknown"		note	"synonym: SCH5.08c"						
/mol_type="unassigned DNA"		complement	(622..2139)						
Query Match		gene	SCH5.08c						
Best Local Similarity		CDS	SCH5.08c						
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		note	"SCH5.08c, possible transferase, len: 505 aa; limited similarity to many proteins of undefined function e.g. TR:027384 (EMBL:AE000896) methyltransferase related protein (196 aa) fasta scores; opt: 162, z-score: 186.2, E(): 0.0046, (28.9% identity in 152 aa overlap). Contains PS00092 N-6 Adenine-specific DNA methylases signature"						
Qy 237 GATCCAGACGGCGGTCTGCGGGTTGAGGTCTCTGGTGCCAGTCCGCTGACGCGAC 296		codon_start	1						
Db 1 GATCCAGACGGCGGTCTGCGGGTTGAGGTCTCTGGTGCCAGTCCGCTGACGCGAC 60		transl_table	11						
Qy 297 GTCGTGCGGCTGGTGTATGCGCGCGCGTAGGCGTCTCGGTCCCAACGTCAGACCGGT 356		product	"putative transferase"						
Db 61 GTCGTGCGGCTGGTGTATGCGCGCGCGTAGGCGTCTCGGTCCCAACGTCAGACCGGT 120		protein_id	"CAB38482.1"						
Qy 357 GCCCGGCGGAT 368		db_xref	"GI:4539563"						
Db 121 GCCCGGCGGAT 132		db_xref	"GOA:Q9X911"						
RESULT 13		db_xref	"UniProt/TREMBL:Q9X911"						
SC0939117		translation	"MSNANSLPSPADRPDVAIRLDALLGASFTADGELLELLGAPAY						
LOCUS		NAALSRSTVPALRATRGDTFLELLVRLFLQQQVPHARVADVLFPVDACLESGLWDHAG							
DEFINITION		309050 bp	DNA						
ACCESSION		complete genome; segment 14/29.	BCT 11-FEB-2003						
AL939117		Streptomyces coelicolor A3(2)	AL049754						
AL035636		AL049731	AL078610						
AL079348									

```

DDVETATVDVRPYGGGGEWVVDLGCAGVGAGGIGNHAEGVILGVGGASTTLAGL
TVTPVSAALDLGTSGIQALHAAAHATVATDVPNPRALHTALTALSGAPAADLR
EGSLFPAADDETDILIVSNPPFVIFGARLTYRDGGMGGDDLCRLSVQOTYERLNEG
GFAHLANQWVEGBEWTOKRLSRWVPHGCCDAMIQREVQDVQIYASLMDLRDAGDRGD
PADYQARYDLAWLDFEARKVAVFGWITILRTGAADPSVVAEEWPHFVQELGETVR
AHPDRVDYLRSHDDAALLAEHAFHTLSGEVVOEQVLPCAEDPHEHVLQRNGRKEATRV
DTVGAGVAGVCDGTMSAGRIILDAIAQLVGEDPVALRDRTPAQIRILLVEQGFLEPA"
complement(1417..1437)
/genes="SCO3545"
/notes="PS00092 N-6 Adenine-specific DNA methylases
signature."
complement(2227..2817)
/genes="SCO3546"
/notes="synonym: SCH5_09c"
complement(2227..2817)
/genes="SCO3546"
/notes="SCH5_09c, possible small lipoprotein, len: 196aa;
Contains PS00013 Prokaryotic membrane lipoprotein lipid
attachment site and probable N-terminal signal sequence.
Contains probable coiled-coil from 104 to 141 (38
residues), max score: 1.630, (probability 1.00)."
/codon_start=1
/transl_table=11
/product="putative small secreted protein"
/protein_id="CAB38483.1"
/db_xref="GI:4539564"
/db_xref="UniProt/TREMBL:Q9X912"
/transl_table=11
/translation="MEGTNPVKKLAALSGGAVLVALTGCSSSDNEKLDLWAKDV
CEGVQKQAEIAAIAIQTETSDNSTPAEVRKTDKAFQDMSDAYKAMGATVQKAGP
PDVDGKKQDAVTELNGLSASVSLRQVEBTDKQAKFADGLKDIATLNLKLSK
SGSNALTKLEGDVGQAWAKQPSCKSASVTPSAEG"
complement(2734..2766)
/genes="SCO3546"
/notes="PS00013 Prokaryotic membrane lipoprotein lipid
attachment site."
complement(3037..5421)
/genes="SCO3547"
/notes="synonym: SCH5_10c"
complement(3037..5421)
/genes="SCO3547"
/notes="SCH5_10c, probable pyrophosphate synthase len: 794
aa; similar to many e.g. TR:O68460 (EMBL:AF044912) H+
translocating pyrophosphate synthase from Rhodospirillum
rubrum (660 aa) fasta scores; opt: 1169, z-score: 1286.1,
E(): 0, (44.6% identity in 697 aa overlap). DNA sequence
contains 35 base inverted repeat with 37 base loop
(15201..15308)."
/codon_start=1
/transl_table=11
/product="putative pyrophosphate synthase"
/protein_id="CAB38484.1"
/db_xref="GI:4539565"
/db_xref="GOA:Q9X913"
/db_xref="UniProt/TREMBL:Q9X913"
/translation="MDELPTSHLAAVLTDGNRALVAVIAVVALAALVAGLVROVL
AAGGTOSMKIAAIVOGANAYLARQLRLGVPVAVVFFLLMLPADDNRQAGRI
FFLLGAAPSAATYIGMWLAVRSNVRVAAAAREATPAPGEPKDLALVSHKATIAFR
TGGVVGFTTGLLACCCVVLVYADAPKVLGFGALALIAMFRVGGIFTKAD
VGADLVKEQGIPEDDPRNAATADNVGNVGCAGMAADLFESAVTLVAALILGK
VAFGDFGLAPLVPAIGLVLTAMIGIFAVAPRRSDRSGMAINRFFISIVLSILVA
VAVVPLPGKVDLDGDDTAIAKSGSDPRLIALVAVALGIVLVAALIQLTGYPTFTT
RRPVDIGKSLTGTPATVVLVAGISIGLESAYVTALLILGLVYGFALGGTSLMALFA
VALAGTLLTTVGVIVAMDTPGVDNAQGAEMSGDVEGAGAVLTLDLQAGNTTKA
ITKGATATVLAALAFSGYRDATITGAADVGEKLSEGAFTMLMDI SOPNNVLG
IAGAAVFLFGLAINAVRSAGAVVEVRQFRPGIMDYSEKPYGKVVDICTDR
ALRELATPGLIAPVAFIFIGTLGVGALGAFAGIAGITLMAVFLANSWGSWNAKK
LVEGHGGKSGSEHAATVIGDTPKDTAGTAIINPLLKNVLIALLIAPVIFKS
YGAOKSVVVRVLIIVAFVAVVAAVYVSKRGIAIGEDDDADPEPKSADPAVVS"
4668..4775
/notes="35 base inverted repeat with possible 37 base
loop."
repeat_region
5559..5564
misc_feature
/notes="Cleavage site for AseI restriction endonuclease"

```

```

AT*TAAT."
complement(5559..5564)
/notes="Cleavage site for AseI restriction endonuclease
AT*TAAT."
complement(5760..6191)
/genes="SCO3548"
/notes="synonym: SCH5_11c"
complement(5760..6191)
/genes="SCO3548"
/notes="SCH5_11c, probable anti-sigma factor, len: 143 aa;
similar to many e.g. SW:RSBW_BACSU RsbW, anti-sigma B
factor from Bacillus subtilis (160 aa) fasta scores; opt:
153, z-score: 198.9, E(): 0.00089, (28.7% identity in 136
aa overlap) and SW:SP22_BACSU SpoIIAB, anti-sigma F
factor, sporulation protein, from Bacillus subtilis (146
aa) fasta scores; opt: 125, z-score: 165.8, E(): 0.063,
(29.2% identity in 137 aa overlap)."
/codon_start=1
/transl_table=11
/product="putative anti-sigma factor"
/protein_id="CAB38485.1"
/db_xref="GI:4539566"
/db_xref="UniProt/TREMBL:Q9X914"
/translation="MATVELRFSALPEHVRTARLVAARVARRAGVDEAVLDEVRLAVG
EACTRAVLGHQHVGITAPVKVSLIEEKQFSIEVGDEAPHAVPGVKTSGDAVDELEAE
EDBMGLAVISGLVDVEVSGEDGGLIRMTPTASAVLPPI"
complement(6301..6642)
/genes="SCO3549"
/notes="synonyms: bldG, SCH5_12c"
complement(6301..6642)
/genes="SCO3549"
/notes="SCH5_12c, bldG, probable anti-sigma factor
antagonist, len: 113 aa; similar to many e.g.
SW:RSBV_BACSU RsbV, anti-sigma B factor antagonist from
Bacillus subtilis (109 aa) fasta scores; opt: 255,
z-score: 341.7, E(): 9.9e-12, (45.7% identity in 94 aa
overlap) and SW:SP21_BACSU spoIIAA, anti-sigma F factor
antagonist (116 aa) fasta scores; opt: 179, z-score:
244.8, E(): 2.5e-06, (30.2% identity in 96 aa overlap)."
/codon_start=1
/transl_table=11
/product="putative anti-sigma factor antagonist"
/protein_id="CAB38486.1"
/db_xref="GI:4539567"
/db_xref="UniProt/Swiss-Prot:Q9WVX8"
/translation="MDLSLSTRVTVGRTVEVGEIDVVTAPKLREQLVNLVNDGSPH
LVVDMGVDPLDSTGLGVLVGLKRVRAHEGSRULVCNQERILKIFRITGLTKVFPPIH
TSVEEAAVAAATD"
6752..9199
/genes="SCO3550"
/notes="synonym: SCH5_13"
Query Match 7.6%; Score 126.6; DB 1; Length 309050;
Best Local Similarity 66.2%; Pred. No. 3.3e-08;
Matches 198; Conservative 0; Mismatches 99; Indels 2; Gaps 1;
Qy 6 ATCTACTCGACCTTCGCGGACCGGGCTACCCGGTGGCTCGCTACTTCGGCCATCCG 65
|||||
84606 ATCGCCGCGACCTTCGCGGAGCGCCCTACCCGGCGGACTGACGTACTTCGGGACCCG 84665
|||||
Qy 66 CTGCGGACCGCTTCGCGGTCGCGACCGATCAACGCGATGGAAGACGAAGGCATCGTGCC 125
|||||
84666 CTGGCTTCGCGCGCGCGCGCTCGCCACCGATCAACGTGATGCGGAGGAGGCGTCTGCGAG 84725
|||||
Qy 126 AACGCTCCCGCATTCGCGGAGCGAGTCTCTCGACCGGGTCTGCGCGATCTCGCGCCCGG 185
|||||
84726 CACGCGCGCGACTTCGCGCGCGAGTCTCTCGAGCGCGCGTTCGCGGAGCTGCGCGAGCGC 84785
|||||
Qy 186 CACCGTTCGTCGCGGAAGTCGCGGCGCTCTTCTGGCG--GGATCTGATCCAG 243
|||||
84786 CACCGAGCGTGGCGGAGGTCGCGGAGACCGGCAATGTTCTGGGCGCTGGAGCTGTCGGG 84845
|||||
Qy 244 AACGGCGCGTCTCGCGGTTGAGGTCTCTCGGTGCCCAGTGCCTCGACGCGACGTCGTC 302
|||||

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 17:41:32 ; Search time 863 Seconds  
(without alignments)  
11352.459 Million cell updates/sec

Title: US-10-607-752-115  
Perfect score: 1655  
Sequence: 1 gatctatctactgaccttc.....atcaccatcaccatcactga 1655

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_16Dec04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

sult No.	Score	Query Match %	Length	DB	ID	Description
1	1655	100.0	1749	5	AAF25122	Aaf25122 Nucleotid
2	1011.4	61.1	1749	5	AAF25120	Aaf25120 Nucleotid
3	740.2	44.7	1749	5	AAF25121	Aaf25121 Nucleotid
4	291	17.6	291	5	AAF25081	Aaf25081 Nucleotid
5	261	15.8	261	5	AAF25084	Aaf25084 Nucleotid
6	226	13.7	697	5	AAF25080	Aaf25080 Nucleotid
7	210	12.7	210	5	AAF25079	Aaf25079 Nucleotid
8	177	10.7	177	5	AAF25087	Aaf25087 Nucleotid
9	147	8.9	147	5	AAF25082	Aaf25082 Nucleotid
10	138	8.3	138	5	AAF25083	Aaf25083 Nucleotid
11	132	8.0	132	5	AAF25086	Aaf25086 Nucleotid
12	114	6.9	114	5	AAF25077	Aaf25077 Nucleotid
13	96	5.8	96	5	AAF25075	Aaf25075 Nucleotid
14	95.6	5.8	1245	11	ABD00374	Abd00374 Klebsiell
15	95.6	5.8	1371	11	ABD00219	Abd00219 Klebsiell
16	95.6	5.7	1338	4	AA553967	Aa553967 Klebsiell
17	87.8	5.3	114955	2	AA53491	Aax53491 Human ade
18	80	4.8	114955	2	AA53491	Aax53491 Human ade
19	75	4.5	75	5	AAF25076	Aaf25076 Nucleotid
20	69.2	4.2	4725	10	AAD55818	Aad55818 Micromono

C	21	69.2	4.2	60196	10	AAD55810	Aad55810 Micromono
	22	68.4	4.1	1314	5	AAH67646	Aah67646 C glutami
	23	68.4	4.1	1330	4	AAF71918	Aaf71918 Corynebac
	24	68.4	4.1	1330	4	AAF72012	Aaf72012 Corynebac
	25	68.4	4.1	1330	4	AAF71905	Aaf71905 Corynebac
	26	68.4	4.1	1330	4	AAF71755	Aaf71755 Corynebac
	27	68.4	4.1	1330	4	AA596078	Aas96078 C. glutam
	28	68.4	4.1	1491	4	AAF71904	Aaf71904 Corynebac
	29	68.4	4.1	1491	4	AAF71917	Aaf71917 Corynebac
	30	68.4	4.1	1491	4	AAF71754	Aaf71754 Corynebac
	31	68.4	4.1	1491	4	AAF72011	Aaf72011 Corynebac
	32	68.4	4.1	1491	4	AA596077	Aas96077 C. glutam
	33	68.4	4.1	1498	10	ADD13562	Add13562 C. glutam
	34	68.4	4.1	349980	5	AAH68532	Aah68532 C glutami
C	35	66.8	4.0	15624	13	ADQ91707	Adq91707 Polyketid
	36	66.8	4.0	164051	13	ADQ91695	Adq91695 Polyketid
C	37	66.2	4.0	1368	13	ADS62019	Ads62019 Bacterial
	38	66.2	4.0	1383	4	AAS51420	Aas51420 Pseudomon
	39	66.2	4.0	1383	8	ACA19524	Aca19524 Prokaryot
	40	66.2	4.0	1413	11	ABD17125	Abd17125 Pseudomon
	41	66.2	4.0	1527	11	ABD17094	Abd17094 Pseudomon
C	42	66.2	4.0	1791	11	ABD17018	Abd17018 Pseudomon
	43	65.2	3.9	1440	8	ACA23916	Aca23916 Prokaryot
C	44	64.4	3.9	1209	8	ABX56043	Abx56043 M. echino
	45	63.4	3.8	14055	8	AAL61170	Aal61170 Actinobeyn

## ALIGNMENTS

RESULT 1  
AAF25122  
ID AAF25122 standard; DNA; 1749 BP.  
XX  
AC AAF25122;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of an 8-mer multi-epitope designated ME/D.  
XX  
KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.  
XX  
OS Synthetic.  
OS Mycobacterium vaccae.  
FH Key Location/Qualifiers  
CDS 1..1749  
FT /\*tag= a  
FT /product= "multi-epitope"  
XX  
XX MO200104140-A1.  
XX  
XX 18-JAN-2001.  
XX  
XX 10-JUL-2000; 2000WO-NZ000121.  
XX  
XX 12-JUL-1999; 99US-00351348.  
XX  
XX 29-NOV-1999; 99US-00450072.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
XX Delcayre A;  
XX  
XX WPI; 2001-168411/17.  
XX  
XX P-PSDB; AAB31660.  
XX  
XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
XX vaccae, useful for treating mycobacterial infections, immune disorders  
XX and cancers.  
XX  
XX Claim 7; Page 68; 80pp; English.  
XX

CC The specification describes an immunogenic epitope of a Mycobacterium  
CC vaccine antigen. The epitope is a stimulator of cytokine production. The  
CC epitopes are useful for the treatment of immune disorders, infectious  
CC diseases, especially tuberculosis, and cancer. They are also useful for  
CC treatment of other mycobacterial infections such as those caused by  
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
CC immune responses, and for producing vaccines. The present sequence  
CC encodes an 8-mer multi-epitope designated ME/D

XX SQ Sequence 1749 BP; 275 A; 612 C; 581 G; 281 T; 0 U; 0 Other;

Query Match 100.0%; Score 1655; DB 5; Length 1749;  
Best Local Similarity 100.0%; Pred. No. 3.3e-297;  
Matches 1655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCTATCTACTCGACCTTCGCGCAGCGGCGGTACCGGGTGGCCCTCAGCTATCTCGGCG 60  
95 GATCTATCTACTCGACCTTCGCGCAGCGGCGGTACCGGGTGGCCCTCAGCTATCTCGGCG 154  
QY 61 ATCCGCTGGCGACCGCTGGCGGTCGCGAGCATCAACCGGATGGAAGAGGAGGATGG 120  
155 ATCCGCTGGCGACCGCTGGCGGTCGCGAGCATCAACCGGATGGAAGAGGAGGATGG 214  
QY 121 TGSCCAACGCTGCCGATCGGCGAGCAGGTGCTCGGACCGGTCGCGGATCTCGCG 180  
215 TGSCCAACGCTGCCGATCGGCGAGCAGGTGCTCGGACCGGTCGCGGATCTCGCG 274  
QY 181 CCGCGCACGCTTCGCTCGGCGAAGTCGCGGCTCGCGCTCTTCGCGCGGATCTGATC 240  
275 CCGCGCACGCTTCGCTCGGCGAAGTCGCGGCTCGCGCTCTTCGCGCGGATCTGATC 334  
QY 241 CAGAACGGGCGGCTTCGCGGTTGAGGTCTCGGTGCGGTCGCGGTCGAGCGGAGCTCG 300  
335 CAGAACGGGCGGCTTCGCGGTTGAGGTCTCGGTGCGGTCGCGGTCGAGCGGAGCTCG 394  
QY 301 TCGCGCTGCTGATCGGCGCGCTAGGCTCTCGGTCCACAACTCAGCAACCGTGCC 360  
395 TCGCGCTGCTGATCGGCGCGCTAGGCTCTCGGTCCACAACTCAGCAACCGTGCC 454  
QY 361 GGGCGGATGGATCTATCAGTTCGGCTTCGTCGCGGCTCGCGGCGGAGCGGAGCTTC 420  
455 GGGCGGATGGATCTATCAGTTCGGCTTCGTCGCGGCTCGCGGCGGAGCGGAGCTTC 514  
QY 421 CTGCGGCTCGATCGGCTGGGTCGCTCGGCGCAGCAGCAGCATCCACCGAGTCCA 480  
515 CTGCGGCTCGATCGGCTGGGTCGCTCGGCGCAGCAGCAGCATCCACCGAGTCCA 574  
QY 481 GCAACGGGTCCTCGACGCTGACATCTCCAGTTCGATGAACCGCGGAGCTCGGGAC 540  
575 GCAACGGGTCCTCGACGCTGACATCTCCAGTTCGATGAACCGCGGAGCTCGGGAC 634  
QY 541 CGCGGCGCAGCAGCAGTTCGATGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCG 600  
635 CGCGGCGCAGCAGCAGTTCGATGCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCG 694  
QY 601 CGTGGGCTCGGCGAGTTCAGCTCGGCGGAGCAGTCAACCGGAGGAGGAGTCCG 660  
695 CGTGGGCTCGGCGAGTTCAGCTCGGCGGAGCAGTCAACCGGAGGAGGAGTCCG 754  
QY 661 GCGCGGATCTGATCAGCTCGGCGGAGCGGCTCGGCGGAGGAGGAGGAGGAGGAG 720  
755 GCGCGGATCTGATCAGCTCGGCGGAGCGGCTCGGCGGAGGAGGAGGAGGAGGAG 814  
QY 721 GAGACGGCGGATGTCGCGGAGCAGCGGCTCGGCGGAGGAGGAGGAGGAGGAGGAG 780  
815 GAGACGGCGGATGTCGCGGAGCAGCGGCTCGGCGGAGGAGGAGGAGGAGGAGGAG 874  
QY 781 CCGCGGACCGGTCGGAGTCAACCGGCGGAGCAGCGGCTCGGCTCGGCTCGGCTCG 840  
875 CCGCGGACCGGTCGGAGTCAACCGGCGGAGCAGCGGCTCGGCTCGGCTCGGCTCG 934  
QY 841 CAGCGGATGGATCTGATCGGCGGAGTCAACCGGAGGAGGAGGAGGAGGAGGAGGAG 900

Db 935 CACGGATGATCTGATCGGCGAGGCATCACGAACAGTAAGCGGTGTTCGGTTGAATCCA 994  
QY 901 ATGTGCTGTACGAGGAGTTCGATCCGAAACACGACGAGGAGTTCGAAATCTGTC 960  
Db 995 ATGTGCTGTACGAGGAGTTCGATCCGAAACACGACGAGGAGTTCGAAATCTGTC 1054  
QY 961 TCGCGACCTTGGCGTCAGCGGCGTTCGCGTCCGAAACCGCGCGGATGTCGCGCG 1020  
1055 TCGCGACCTTGGCGTCAGCGGCGTTCGCGTCCGAAACCGCGCGGATGTCGCGCG 1114  
QY 1021 CGCTGCGGCGCGCTCTCCATGCGCGGTTCTGTTCACTGCTGCTGCGGTGCTGTTCTGC 1080  
1115 CGCTGCGGCGCGCTCTCCATGCGCGGTTCTGTTCACTGCTGCTGCGGTGCTGTTCTGC 1174  
QY 1081 GAAAGGCGCGCGCGCTGCTGCTGCGATACGCGGATCTATACGAGGATGAGCGCTC 1140  
1175 GAAAGGCGCGCGCGCTGCTGCTGCGATACGCGGATCTATACGAGGATGAGCGCTC 1234  
QY 1141 CAGCGCTACTCTTCGCGCGCAGAACAGCGTTCGCGCGGAGCAGCGGTCCTGCG 1200  
1235 CAGCGCTACTCTTCGCGCGCAGAACAGCGTTCGCGCGGAGCAGCGGTCCTGCG 1294  
QY 1201 GCCAGATACACCGAGCGGTCGCGGATGTCAGATCGTGGCGAGCGCGCGGACAG 1260  
1295 GCCAGATACACCGAGCGGTCGCGGATGTCAGATCGTGGCGAGCGCGCGGACAG 1354  
QY 1261 TGGAGATCGGATCTATCGCGCGCTGTCGCGGAGGAGCAGCGGTCGAGGCTGTCAC 1320  
1355 TGGAGATCGGATCTATCGCGCGCTGTCGCGGAGGAGCAGCGGTCGAGGCTGTCAC 1414  
QY 1321 AGTTCGCGCGGTCGCGAGAGAGGAGCTACATCGACGAGGCTTTCGCAACATCGGG 1380  
1415 AGTTCGCGCGGTCGCGAGAGAGGAGCTACATCGACGAGGCTTTCGCAACATCGGG 1474  
QY 1381 CGTATCTGCGAGCTGAGGTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
1475 CGTATCTGCGAGCTGAGGTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1534  
QY 1441 CCGGACCGCGTGGATCGTTCTGCTAGTACCGGAGCTCTTGAGAGTAAAGGCAATTGG 1500  
1535 CCGGACCGCGTGGATCGTTCTGCTAGTACCGGAGCTCTTGAGAGTAAAGGCAATTGG 1594  
QY 1501 AAGATCTTGGACCTTCCATCAATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560  
1595 AAGATCTTGGACCTTCCATCAATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1654  
QY 1561 GCGCGGCTTTCGAGTGAACCTTGGGCGAGGCAATCCCATCGCGCGAGCGCGGAGCG 1620  
1655 GCGCGGCTTTCGAGTGAACCTTGGGCGAGGCAATCCCATCGCGCGAGCGCGGAGCG 1714  
QY 1621 AAATCCACGGATCCCATCAGGATCAGGATCAGGATCAGGATCAGGATCAGGAT 1655  
1715 AAATCCACGGATCCCATCAGGATCAGGATCAGGATCAGGATCAGGATCAGGAT 1749

RESULT 2

AAF25120

ID AAF25120 standard; DNA; 1749 BP.

XX AAF25120;

AC AAF25120;

XX 30-APR-2001 (first entry)

DT 30-APR-2001 (first entry)

XX Nucleotide sequence of an 8-mer multi-epitope designated ME/A.

DE Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.

XX Synthetic.

OS Mycobacterium vaccae.

XX Key

XX Location/Qualifiers

FT 1. .1749

```

PT  /*tag= a
XX  /product= "multi-epitope"
PN  W0200104140-A1.
XX  18-JAN-2001.
XX  10-JUL-2000; 2000WO-NZ000121.
XX  12-JUL-1999. 99US-00351348.
PR  29-NOV-1999; 99US-00450072.
XX  (GENE-) GENESIS RES & DEV CORP LTD.
XX  Delcayre A;
XX  WPI; 2001-168411/17.
DR  P-PSDB; AAB31658.
XX  Novel polypeptides comprising immunogenic epitopes of Mycobacterium
PT  vaccae, useful for treating mycobacterial infections, immune disorders
XX  and cancers.
XX  Claim 7; Page 66-67; 80pp; English.
XX  The specification describes an immunogenic epitope of a Mycobacterium
CC  vaccae antigen. The epitope is a stimulator of cytokine production. The
CC  epitopes are useful for the treatment of immune disorders, infectious
CC  diseases, especially tuberculosis, and cancer. They are also useful for
CC  treatment of other mycobacterial infections such as those caused by
CC  Mycobacterium avium. The epitopes are especially useful for inducing TH1
CC  immune responses, and for producing vaccines. The present sequence
CC  encodes an 8-mer multi-epitope designated ME/A
XX  SQ Sequence 1749 BP; 275 A; 612 C; 581 G; 281 T; 0 U; 0 Other;
Query Match 61.1%; Score 1011.4; DB 5; Length 1749;
Best Local Similarity 78.9%; Pred. No. 4.4e-178;
Matches 132; Conservative 0; Mismatches 236; Indels 60; Gaps 8;
Qy 1 GATCTATCTACTCGACCTTCGCGACCGGGGTACCGGGTGGCTGACCTACTCGGGCC 60
Db 95 GATCTATCTACTCGACCTTCGCGACCGGGGTACCGGGTGGCTGACCTACTCGGGCC 154
Qy 61 ATCCGCTGGGACCGCTTCGCGACCGGGGTACCGGGTGGCTGACCTACTCGGGCC 120
Db 155 ATCCGCTGGGACCGCTTCGCGACCGGGGTACCGGGTGGCTGACCTACTCGGGCC 214
Qy 121 TGGCCAAAGCTGCGCGATCGCGACGAGGTGCTCGGACCGGGTCTCGCGATCTCGCG 180
Db 215 TGGCCAAAGCTGCGCGATCGCGACGAGGTGCTCGGACCGGGTCTCGCGATCTCGCG 274
Qy 181 CCCGGCACCGTTCGCTGGGAAAGTTCGCGCGCTTCGCGGTCTTCGCGCGGATCTGATC 240
Db 275 CCCGGCACCGTTCGCTGGGAAAGTTCGCGCGCTTCGCGGTCTTCGCGCGGATCTGATC 334
Qy 241 CAGAACCGGCGGTTCGCGGTTCGAGGTCTCGGTGCGCGGTTCGCGGTTCGCGGTTCGCG 300
Db 335 CAGAACCGGCGGTTCGCGGTTCGAGGTCTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCG 394
Qy 301 TCGCGCTGGTGTGATCGCGCGCGCTAGCGCTTCGCGGTTCGCGGTTCGCGGTTCGCGGT 360
Db 395 TCGCGCTGGTGTGATCGCGCGCGCTAGCGCTTCGCGGTTCGCGGTTCGCGGTTCGCGGT 454
Qy 361 GGGCGGATGATCTATCAGTTTCGCGCTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 420
Db 455 GGGCGGATGATCTATCAGTTTCGCGCTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 510
Qy 421 CTCGCGGTTCGATTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 480
Db 511 TCCAAATGTGCTGATCAGGAGGATCCGA-----TGCCGAAACACCGACCGCGAGGATC 564
Qy 481 GCAACGGGTCCCGACCGGTGCACATCTCCAGTTCGATGAAACCGCGCGAGCTCGGGGAGT 540

```

```

565 GCAATCTGTCTCGCGACCTTCGCGTCAACCGCGCGTTCGCGTTCGCGTTCGCGTTCGCGT 624
541 CGCGCGCGACGACGAGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGT 600
625 GTGCGCGCGCGCT-----GCGCGCGCGCTTCGCGTTCGCGTTCGCGTTCGCGT 671
601 CGTTCGCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 660
672 CGTTCGCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 724
661 GCGCGGATCTGATCAGCTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 720
725 ATACCGGATCTGATCAGCTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 784
721 GAGACCGCGCGATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
785 GAGACCGCGCGCGATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 844
781 CGCGGACCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 840
845 CGCGGACCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 904
841 CACCGGATGATCT-----GATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 896
905 CACCGGATGATCTATCAGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 964
897 TCCAAATGCTCTGACGACGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTC 950
965 CTCGCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTC 1024
951 GCAATCTGTCTCGCGACCTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 1010
1025 GCAACGGGTCCCGACCGGTGCATCTCCAGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 1084
1011 GTGCGCGCGCGCT-----GCGCGCGCGCTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 1057
1085 CGCGCGCGACGACGAGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGCGT 1144
1058 CGTCTGCTGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 1110
1145 CGTTCGCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 1204
1111 ATACCGGATCTATCAGCGAGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTC 1170
1205 GCGCGGATCTATCAGCGAGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCG 1264
1171 GCGTTCGCGCGCGACGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 1230
1265 GCGTTCGCGCGCGACGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 1324
1231 TCCAGATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1290
1325 TCCAGATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1384
1291 GGAAGACGAGCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCG 1350
1385 GGAAGACGAGCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCG 1444
1351 ACATCGACCGCGCTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 1410
1445 ACATCGACCGCGCTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 1504
1411 TCCAGATCTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1470
1505 TCGGATCTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1564
1471 CGAAGCTCTTGAGAGCTTAAGGCGCAATTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCG 1530
1565 CGAAGCTCTTGAGAGCTTAAGGCGCAATTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCG 1624
1531 AAAAGCATCGCCCTAGGGGATTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCG 1590

```

Db 1625 AAAAGCATCCCTAGGGATCCGTAGCGGCCCGGGTGTTCAGTGAACATTGGGCGAGG 1684  
 QY 1591 CAATCCATCCGCGCGAGCCCGCGGCGGGAATCCACGGATCCCATCACCATC 1650  
 Db 1685 CAATCCATCCGCGCGAGCCCGCGGCGGGAATCCACGGATCCCATCACCATC 1744  
 QY 1651 ACTGA 1655  
 Db 1745 ACTGA 1749

RESULT 3  
 AAF25121  
 ID AAF25121 standard; DNA; 1749 BP.  
 XX  
 AC AAF25121;  
 30-APR-2001 (first entry)  
 DE Nucleotide sequence of an 8-mer multi-epitope designated ME/B.  
 XX  
 KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
 KW cancer; mycobacterial infection; Th1 immune response; vaccine; ss.  
 XX  
 OS Synthetic.  
 OS Mycobacterium vaccae.

XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1749  
 FT /\*tag= a  
 FT /product= "multi-epitope"

XX WO200104140-A1.  
 XX 18-JAN-2001.  
 XX 10-JUL-2000; 2000WO-NZ000121.  
 XX 12-JUL-1999; 99US-00351348.  
 PR 29-NOV-1999; 99US-00450072.  
 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 PA Delcayre A;  
 PI WPI; 2001-168411/17.  
 P-PSDB; AAB31659.

XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
 PT vaccae, useful for treating mycobacterial infections, immune disorders  
 PT and cancers.

XX Claim 7; Page 67; 80pp; English.  
 XX The specification describes an immunogenic epitope of a Mycobacterium  
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
 CC epitopes are useful for the treatment of immune disorders, infectious  
 CC diseases, especially tuberculosis, and cancer. They are also useful for  
 CC treatment of other mycobacterial infections such as those caused by  
 CC Mycobacterium avium. The epitopes are especially useful for inducing Th1  
 CC immune responses, and for producing vaccines. The present sequence  
 CC encodes an 8-mer multi-epitope designated ME/B

XX Sequence 1749 BP; 275 A; 612 C; 581 G; 281 T; 0 U; 0 Other;  
 Query Match 44.7%; Score 740.2; DB 5; Length 1749;  
 Best Local Similarity 69.0%; Pred. No. 6.9e-128;  
 Matches 1244; Conservative 0; Mismatches 263; Indels 296; Gaps 5;

QY 1 GATCTATCTACTGACCTTCGCGAGCGGCGGTACCGGGTGGCTGACGTACTCGGCC 60  
 Db 95 GATCTATCTACTGACCTTCGCGAGCGGCGGTACCGGGTGGCTGACGTACTCGGCC 154

QY 61 ATCCGCTGCGCAGCCGCTGCGGGTCCGAGCATCAACGCGATGGAAGACGAGCATGG 120  
 Db 155 ATCCGCTGCGCAGCCGCTGCGGGTCCGAGCATCAACGATGGAAGACGAGCATGG 214  
 QY 121 TGGCCAAACGCTCCCGCGCATCGGCGAGCAGGTGCTCGGACCGGGTCTCGCGCATCTCGCG 180  
 Db 215 TGGCCAAACGCTCCCGCGCATCGGCGAGCAGGTGCTCGGACCGGGTCTCGCGCATCTCGCG 274  
 QY 181 CCGCGCAGCGTTCCGTCGCGGAGTCCGCGGCTCGGCGTCTTCTGGGGGGGATCTGATC 240  
 Db 275 CCGCGCAGCGTTCCGTCGCGGAGTCCGCGGCTCGGCGTCTTCTGGGGG----- 324  
 QY 241 CAGAACGGGCGGCTCTCGGGGTTGAGGTCCTCGGTGCCCAGTGCCTGACGCGAGCTCG 300  
 Db 325 ----- 324  
 QY 301 TCGGGCTGTGATGGCGCGCGGTAGGCGTCTCGGTCCACACGTACAGACCGTGC 360  
 Db 325 ----- 324  
 QY 361 GGGCGGATGGATCTATCAGTTCCGGCCCTGGTCCGAGCCCGCGGAGGCGAGTTCG 420  
 Db 325 -----GGATCTATCAGTTCCGGCCCTGGTCCGAGCCCGCGGAGGCGAGTTCG 376  
 QY 421 CTCGGGCTCGATCGGTTGGGTTCGTCGCGGACGACACAGCATCCACCCGAGTCCA 480  
 Db 377 CTCGGGCTCGATCGGTTGGGTTCGTCGCGGACGACACAGCATCCACCCGAGTCCA 436  
 QY 481 GCAACGGGTTCCCGACGGTGCACATCTCCAGTTCGATGAACCCCGAGTCCGGGACGT 540  
 Db 437 GCAACGGGTTCCCGACGGTGCACATCTCCAGTTCGATGAACCCCGAGTCCGGGACGT 496  
 QY 541 CCGGGCGCAGCAGCAGTTCAGATGCGCAGTCCCGTGCATGATCCCGGGTTCGGCGT 600  
 Db 497 CCGGGCGCAGCAGCAGTTCAGATGCGCAGTCCCGTGCATGATCCCGGGTTCGGCGT 556  
 QY 601 CGTCGGGCTCGCGAGTCCAGCCAGTCCGCGAGCAGCATGACACCGAGGAAACGACTCGG 660  
 Db 557 CGTCGGGCTCGCGAGTCCAGCCAGTCCGCGAGCAGCATGACACCGAGGAAACGACTCGG 616  
 QY 661 GCGCGGATCTGATCAGTTCGGGAGCCGGTCCCGAGAACCGCAGCGTGGGAGACAC 720  
 Db 617 GCGCGGATCTGATC-----GGCAGGATCAGCAACAGTAAAGCGGTTCGCGTT 666  
 QY 721 GAGACGGGCGCATGTCGCGGAGCAGCGCCAGCGTGCACCCCGCGGACCGGCG 780  
 Db 667 GAATCCAAATGTCTGTTCAGCAGGCAATCGATCCGAGAACACCGCAGCAGTTCGCA 726  
 QY 781 CCGCGGACCGCGTCGCGAGTCCGACCCCGCGCAGCCGCGCGCGGTGTGTCAGCATCAGC 840  
 Db 727 ATCTGTCTCGCAACCTTGGGTCACCGGGGTCTCGTGGTCCCGAACCCCGCGCGATGTC 786  
 QY 841 CACGGGATGATCTGATCGGAGGC-----ATCAGAACAGTAAGCGGTGTTCGGTTGAAT 897  
 Db 787 GCGCGCGCGTCTCGCGCGGCTCTCCATGGCGGTTCTGTTCACTGCTGCTCGCGTGGCT 846  
 QY 898 CCAATGTGTGTTCAGCAGCATCCGATGCCGAAACCGACACCGCGAGCAGTTCGCAATCT 957  
 Db 847 GTTCTCGAAACCGGCGCGCGCGTCCGTCGTCGATACCGGATCTGATCAGTTCGGG 906  
 QY 958 GTTCTCGCAACCTGCGGTCAACCGGCGTCCGCAACCCCGCGCGCATGTGCGCG 1017  
 Db 907 GAGCGGGTCCCGAGCAACCGCGTGGGAGACCGAGACCGGGCGCATGTGCGCGG 966  
 QY 1018 GCGCGCTGCGCGCGCTCTCCATGGCGGTTCTGTTAGTCTGCTCGTTCGGTGGCTGTTTC 1077  
 Db 967 CAGCAGCGCGCAGCGTGTACCCCGCGGAGCCCGCGGACCGCGGATCGGAGTTCGAC 1026  
 QY 1078 TCGGAAACGGGCGCGCGCG-----CGTGTCTCGTCCGATACCGGATCTATCAGCAG 1130  
 Db 1027 CCGGCGCGCACCGCGCGCGGTGTGATGATACAGCAGCGGATGATCTATCAGCAG 1086  
 QY 1131 GTAGGCGTCCAGCGGTACTCTTCGCCCCAGAACAGCGGTGCCGTGCGCGCGAGACCG 1190

Db 1087 GTAGCGCTCCAGCGTACTCTTCGCGCCAGAAACAGCGGTCCGTCGCGCGCAGACCA 1146  
 Qy 1191 CGGTCTTCGCGCAGATACACCCAGCGGTGGCGGCATGTCCAGATCTGTGGCCAGCGG 1250  
 Db 1147 CGGTCTTCGCGCAGATACACCCAGCGGTGGCGGCATGTCCAGATCTGTGGCCAGCGG 1206  
 Qy 1251 CGCGGACCGTGGAGATCGGATCTATCGCGCGCTGTGGGGAAGGACGAGGCGGTAGCG 1310  
 Db 1207 CGCGGACCGTGGAGATCGGATCTATCGCGCGCTGTGGGGAAGGACGAGGCGGTAGCG 1266  
 Qy 1311 GCGTTGCACTACGTGCGCCCGTGGCGGAAGGACGAGATCTATCGACGAGCCTTGGCG 1370  
 Db 1267 GCGTTGCACTACGTGCGCCCGTGGCGGAAGGACGAGATCTATCGACGAGCCTTGGCG 1326  
 Qy 1371 AACATCGGCGCTATCTGCGAGCTGAGTTCGCGCTCTGCTGCG----- 1413  
 Db 1327 AACATCGGCGCTATCTGCGAGCTGAGTTCGCGCTCTGCTGCGATCTGATCAGAACGG 1386  
 Qy 1414 ----- 1413  
 Db 1387 GCCGCTCGCGGTTGAGTCTCTCGGTGCCAGTGCCTGCGACGCGACGTCTGTCGGGCT 1446  
 1414 ----- 1413  
 Db 1447 GGTGATCGCGCGCGTAGCGTCTCGGTCCACACGTGAGCAACGTCGCGCGCGGAT 1506  
 Qy 1414 -GATCTATCCCGCCAGCGCGCGGTGCGCGGACCGCGTGGATCTGTCAGTACCGG 1472  
 Db 1507 GGATCTATCGCGCGCACCGCGCGGTGCGCGGACCGCGTGGATCTGTCAGTACCGG 1566  
 Qy 1473 AAGCTCTTGAGAGCTAAGGCAATTGGGAAGATCTTGGACCTTCCCATCAATAGAGGAA 1532  
 Db 1567 AAGCTCTTGAGAGCTAAGGCAATTGGGAAGATCTTGGACCTTCCCATCAATAGAGGAA 1626  
 Qy 1533 AAGCATCGCCCTAGGGGATCCGTAGCGGCGCCGCGTGTTCGAGTGAATTTGGGCGAGGCA 1592  
 Db 1627 AAGCATCGCCCTAGGGGATCCGTAGCGGCGCCGCGTGTTCGAGTGAATTTGGGCGAGGCA 1686  
 Qy 1593 ATCCCATCGCGGAGCGCGGACGGAATCCACGGATCCCATCACCATCAC 1652  
 Db 1687 ATCCCATCGCGGAGCGCGGACGGAATCCACGGATCCCATCACCATCAC 1746  
 Qy 1653 TGA 1655  
 Db 1747 TGA 1749

RESULT 4  
 AAF25081  
 AAF25081 standard; DNA; 291 BP.  
 AC AAF25081;  
 DT 30-APR-2001 (first entry)  
 DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA26.  
 KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
 KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.  
 OS Mycobacterium vaccae.  
 XX WO200104140-A1.  
 XX 18-JAN-2001.  
 XX 10-JUL-2000; 2000WO-NZ000121.  
 XX 12-JUL-1999; 99US-00351348.  
 XX 29-NOV-1999; 99US-00450072.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.

XX Delcayre A;  
 XX WPI; 2001-168411/17.  
 DR P-PSDB; AAB31651.  
 XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
 PT vaccae, useful for treating mycobacterial infections, immune disorders  
 PT and cancers.  
 XX Claim 4; Page 59; 80pp; English.  
 PS The specification describes an immunogenic epitope of a Mycobacterium  
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
 CC epitopes are useful for the treatment of immune disorders, infectious  
 CC diseases, especially tuberculosis, and cancer. They are also useful for  
 CC treatment of other mycobacterial infections such as those caused by  
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
 CC immune responses, and for producing vaccines. The present sequence  
 CC encodes a M. vaccae epitope of the invention  
 XX  
 SQ Sequence 291 BP; 45 A; 103 C; 101 G; 42 T; 0 U; 0 Other;  
 Query Match 17.6%; Score 291; DB 5; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-45;  
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 375 ATCAGTTCCGCGCTGTCGCGCAGCGCGGAGGCGAGCCAGTTCCGTCGCGGTCGATC 434  
 Db 1 ATCAGTTCCGCGCTGTCGCGCAGCGCGGAGGCGAGCCAGTTCCGTCGCGGTCGATC 60  
 Qy 435 GGGTTGGGTCGCTCCGCGCAGCACACAGCATCCACCGAGGTCGAGCAACGGGTCCCG 494  
 Db 61 GGGTTGGGTCGCTCCGCGCAGCACACAGCATCCACCGAGGTCGAGCAACGGGTCCCG 120  
 Qy 495 ACGTGTGCATCTCCCGAGTCGATGAACGCGCGCAGCTCCGGGACGTCCGCGCAGCAGC 554  
 Db 121 ACGTGTGCATCTCCCGAGTCGATGAACGCGCGCAGCTCCGGGACGTCCGCGCAGCAGC 180  
 Qy 555 ACGTGTGCATGAGGCGAGTCGCGTCGATGATCCCGGTTTCGCGCTCGCGGCTCGCG 614  
 Db 181 ACGTGTGTCAGATGGCAGTCGCGTCGATGATCCCGGTTTCGCGCTCGCGGCTCGCG 240  
 Qy 615 GAGTCCAGCGAGTCGCGGAGCACATGACACCGAGGAAACGACTCGGCGCGG 665  
 Db 241 GAGTCCAGCGAGTCGCGGAGCACATGACACCGAGGAAACGACTCGGCGCGG 291

RESULT 5  
 AAF25084  
 ID AAF25084 standard; DNA; 261 BP.  
 XX  
 AC AAF25084;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA37.  
 KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
 KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.  
 XX Mycobacterium vaccae.  
 XX WO200104140-A1.  
 XX 18-JAN-2001.  
 XX 10-JUL-2000; 2000WO-NZ000121.  
 XX 12-JUL-1999; 99US-00351348.  
 XX 29-NOV-1999; 99US-00450072.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.



PA (GENE-) GENESIS RES & DEV CORP LTD.  
 XX Delcayre A;  
 PI WPI; 2001-168411/17.  
 DR P-PSDB; AAB31648.  
 DR Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
 XX vaccae, useful for treating mycobacterial infections, immune disorders  
 PT and cancers.  
 PT Claim 4; Page 59; 80pp; English.  
 XX The specification describes an immunogenic epitope of a Mycobacterium  
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
 CC epitopes are useful for the treatment of immune disorders, infectious  
 CC diseases, especially tuberculosis, and cancer. They are also useful for  
 CC treatment of other mycobacterial infections such as those caused by  
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
 CC immune responses, and for producing vaccines. The present sequence  
 CC encodes a M. vaccae epitope of the invention  
 XX Sequence 210 BP; 45 A; 66 C; 64 G; 35 T; 0 U; 0 Other;  
 SQ Query Match 12.7%; Score 210; DB 5; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-30;  
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1419 ATCGCCGCCACCGCGCGTGCCTGGGCAACCGCGTGGATCGTTCTCAGTACCCGAAAGCTC 1478  
 DB 1 ATCGCCGCCACCGCGCGTGCCTGGGCAACCGCGTGGATCGTTCTCAGTACCCGAAAGCTC 60  
 QY 1479 TTGAGAGCTAAGGCCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGGAAAGCAT 1538  
 DB 61 TTGAGAGCTAAGGCCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGGAAAGCAT 120  
 QY 1539 CGCCTAGGGGATCCGTAGCGGGCCCGTGTTCGAGTGAATTTGGGCGAGGCAATCCCA 1598  
 DB 121 CGCCTAGGGGATCCGTAGCGGGCCCGTGTTCGAGTGAATTTGGGCGAGGCAATCCCA 180  
 QY 1599 TCGCGCGCAGCCCGCGCAGCGGAATCCAC 1628  
 DB 181 TCGCGCGCAGCCCGCGCAGCGGAATCCAC 210  
 RESULT 8  
 AAF25087  
 ID AAF25087 standard; DNA; 177 BP.  
 XX AAF25087;  
 XX 30-APR-2001 (first entry)  
 DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA45.  
 XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
 KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.  
 XX Mycobacterium vaccae.  
 OS WO200104140-A1.  
 PN 18-JAN-2001.  
 PD 10-JUL-2000; 2000WO-NZ000121.  
 PF 12-JUL-1999; 99US-00351348.  
 PR 29-NOV-1999; 99US-00450072.  
 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 PA Delcayre A;  
 PI WPI; 2001-168411/17.  
 DR P-PSDB; AAB31651.  
 DR Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
 XX vaccae, useful for treating mycobacterial infections, immune disorders  
 PT and cancers.  
 PT Claim 4; Page 60; 80pp; English.  
 XX The specification describes an immunogenic epitope of a Mycobacterium  
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
 CC epitopes are useful for the treatment of immune disorders, infectious  
 CC diseases, especially tuberculosis, and cancer. They are also useful for  
 CC treatment of other mycobacterial infections such as those caused by  
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
 CC immune responses, and for producing vaccines. The present sequence  
 CC encodes a M. vaccae epitope of the invention  
 XX Sequence 177 BP; 27 A; 71 C; 66 G; 13 T; 0 U; 0 Other;  
 SQ Query Match 10.7%; Score 177; DB 5; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-23;  
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 672 GATCAGCTCGGGAGCCGGTGCCTCCAGCAACGCCAGCTGGGGAAGCACCCGAGACCGCGC 731  
 DB 1 GATCAGCTCGGGAGCCGGTGCCTCCAGCAACGCCAGCTGGGGAAGCACCCGAGACCGCGC 60  
 QY 732 GATGTCGCCGCGCAGCAGCGCCAGCGCTGCACCCCGCGGACCGGCGCCCGGACCGC 791  
 DB 61 GATGTCGCCGCGCAGCAGCGCCAGCGCTGCACCCCGCGGACCGGCGCCCGGACCGC 120  
 QY 792 GTCGGAGTGCACCCCGCGCGCCACCGCGCGCTGGTTCAGCATCAGCCACCGGAT 848  
 DB 121 GTCGGAGTGCACCCCGCGCGCCACCGCGCGCTGGTTCAGCATCAGCCACCGGAT 177

DR WPI; 2001-168411/17.  
 DR P-PSDB; AAB31656.  
 XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
 PT vaccae, useful for treating mycobacterial infections, immune disorders  
 PT and cancers.  
 PT Claim 4; Page 60; 80pp; English.  
 XX The specification describes an immunogenic epitope of a Mycobacterium  
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
 CC epitopes are useful for the treatment of immune disorders, infectious  
 CC diseases, especially tuberculosis, and cancer. They are also useful for  
 CC treatment of other mycobacterial infections such as those caused by  
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
 CC immune responses, and for producing vaccines. The present sequence  
 CC encodes a M. vaccae epitope of the invention  
 XX Sequence 177 BP; 27 A; 71 C; 66 G; 13 T; 0 U; 0 Other;  
 SQ Query Match 10.7%; Score 177; DB 5; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-23;  
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 672 GATCAGCTCGGGAGCCGGTGCCTCCAGCAACGCCAGCTGGGGAAGCACCCGAGACCGCGC 731  
 DB 1 GATCAGCTCGGGAGCCGGTGCCTCCAGCAACGCCAGCTGGGGAAGCACCCGAGACCGCGC 60  
 QY 732 GATGTCGCCGCGCAGCAGCGCCAGCGCTGCACCCCGCGGACCGGCGCCCGGACCGC 791  
 DB 61 GATGTCGCCGCGCAGCAGCGCCAGCGCTGCACCCCGCGGACCGGCGCCCGGACCGC 120  
 QY 792 GTCGGAGTGCACCCCGCGCGCCACCGCGCGCTGGTTCAGCATCAGCCACCGGAT 848  
 DB 121 GTCGGAGTGCACCCCGCGCGCCACCGCGCGCTGGTTCAGCATCAGCCACCGGAT 177  
 RESULT 9  
 AAF25082  
 ID AAF25082 standard; DNA; 147 BP.  
 XX AAF25082;  
 XX 30-APR-2001 (first entry)  
 DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA27.  
 XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
 KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.  
 XX Mycobacterium vaccae.  
 OS WO200104140-A1.  
 PN 18-JAN-2001.  
 PD 10-JUL-2000; 2000WO-NZ000121.  
 PF 12-JUL-1999; 99US-00351348.  
 PR 29-NOV-1999; 99US-00450072.  
 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 PA Delcayre A;  
 PI WPI; 2001-168411/17.  
 DR P-PSDB; AAB31651.  
 DR Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
 XX vaccae, useful for treating mycobacterial infections, immune disorders  
 PT and cancers.  
 PT Claim 4; Page 59; 80pp; English.

XX The specification describes an immunogenic epitope of a Mycobacterium  
CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
CC epitopes are useful for the treatment of immune disorders, infectious  
CC diseases, especially tuberculosis, and cancer. They are also useful for  
CC treatment of other mycobacterial infections such as those caused by  
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
CC immune responses, and for producing vaccines. The present sequence  
CC encodes a M. vaccae epitope of the invention  
XX  
SQ Sequence 147 BP; 25 A; 54 C; 49 G; 19 T; 0 U; 0 Other;  
Query Match 8.9%; Score 147; DB 5; Length 147;  
Best Local Similarity 100.0%; Pred. No. 4.3e-18;  
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1122 ATCAGCAGGTAGCGGTCCAGCGTACTTTCCGCCAGAAACAGCGGTGCCGCGC 1181  
1 ATCAGCAGGTAGCGGTCCAGCGTACTTTCCGCCAGAAACAGCGGTGCCGCGC 60  
QY 1182 GCAGACGCGGTCTCTCCGCCAGATACACCCAGCGGTGCCGCGATGTCAGATCGTG 1241  
61 GCAGACGCGGTCTCTCCGCCAGATACACCCAGCGGTGCCGCGATGTCAGATCGTG 120  
QY 1242 GCCAGCGCGCGCGCACGGTGGAGATC 1268  
121 GCCAGCGCGCGCGCACGGTGGAGATC 147  
Db  
RESULT 10  
AAF25083  
ID AAF25083 standard; DNA; 138 BP.  
XX  
AC AAF25083;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA29.  
XX  
KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.  
XX  
OS Mycobacterium vaccae.  
XX  
PN WO200104140-A1.  
XX  
PD 18-JAN-2001.  
XX  
PF 10-JUL-2000; 2000WO-NZ000121.  
XX  
PR 12-JUL-1999; 99US-00351348.  
PR 29-NOV-1999; 99US-00450072.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
PI Delcayre A;  
XX  
DR WPI; 2001-168411/17.  
DR P-PSDB; AAB31652.  
XX  
PT Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
PT vaccae, useful for treating mycobacterial infections, immune disorders  
PT and cancers.  
XX  
PS Claim 4; Page 60; 80pp; English.  
XX  
CC The specification describes an immunogenic epitope of a Mycobacterium  
CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
CC epitopes are useful for the treatment of immune disorders, infectious  
CC diseases, especially tuberculosis, and cancer. They are also useful for  
CC treatment of other mycobacterial infections such as those caused by  
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
CC immune responses, and for producing vaccines. The present sequence  
CC encodes a M. vaccae epitope of the invention  
XX  
SQ Sequence 132 BP; 16 A; 44 C; 50 G; 22 T; 0 U; 0 Other;  
Query Match 8.0%; Score 132; DB 5; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.6e-15;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC encodes a M. vaccae epitope of the invention  
XX  
SQ Sequence 138 BP; 23 A; 44 C; 47 G; 24 T; 0 U; 0 Other;  
Query Match 8.3%; Score 138; DB 5; Length 138;  
Best Local Similarity 100.0%; Pred. No. 2e-16;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1275 ATCGCGCGCTGTGGGGAAGACGAGCGGTAGCGGCTTGCACTACGTCGCCCGGTT 1334  
1 ATCGCGCGCTGTGGGGAAGACGAGCGGTAGCGGCTTGCACTACGTCGCCCGGTT 60  
Db  
QY 1335 GCGGAGAAGCAGGACTACATCGACCGAGCTTGGCAACATCGGGCGGTATCTGCCAGCT 1394  
61 GCGGAGAAGCAGGACTACATCGACCGAGCTTGGCAACATCGGGCGGTATCTGCCAGCT 120  
QY 1395 GAGGTTCCCGCTCTCGTC 1412  
121 GAGGTTCCCGCTCTCGTC 138  
Db  
RESULT 11  
AAF25086  
ID AAF25086 standard; DNA; 132 BP.  
XX  
AC AAF25086;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA44.  
XX  
KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.  
XX  
OS Mycobacterium vaccae.  
XX  
PN WO200104140-A1.  
XX  
PD 18-JAN-2001.  
XX  
PF 10-JUL-2000; 2000WO-NZ000121.  
XX  
PR 12-JUL-1999; 99US-00351348.  
PR 29-NOV-1999; 99US-00450072.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
PI Delcayre A;  
XX  
DR WPI; 2001-168411/17.  
DR P-PSDB; AAB31655.  
XX  
PT Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
PT vaccae, useful for treating mycobacterial infections, immune disorders  
PT and cancers.  
XX  
PS Claim 4; Page 60; 80pp; English.  
XX  
CC The specification describes an immunogenic epitope of a Mycobacterium  
CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
CC epitopes are useful for the treatment of immune disorders, infectious  
CC diseases, especially tuberculosis, and cancer. They are also useful for  
CC treatment of other mycobacterial infections such as those caused by  
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
CC immune responses, and for producing vaccines. The present sequence  
CC encodes a M. vaccae epitope of the invention  
XX  
SQ Sequence 132 BP; 16 A; 44 C; 50 G; 22 T; 0 U; 0 Other;  
Query Match 8.0%; Score 132; DB 5; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.6e-15;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



KW Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.

XX Klebsiella pneumoniae.

XX US6610836-B1.

XX 26-AUG-2003.

XX 27-JAN-2000; 2000US-00489039.

XX 29-JAN-1999; 99US-0117747P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton GL, Osborne M;

XX WPI; 2003-895346/82.

XX P-PSDB; ABO66803.

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.

XX Disclosure; SEQ ID NO 6149; 932pp; English.

XX The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae polypeptide of the invention

XX Sequence 1245 BP; 229 A; 431 C; 380 G; 205 T; 0 U; 0 Other;

Query Match 5.8%; Score 95.6; DB 11; Length 1245;

Best Local Similarity 65.4%; Pred. No. 1.4e-08;

Matches 140; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 17 CTTGCGGACCGGGCTACCGGGTGGCTGACGTACTCGGCATCCGCTGGCGACCGC 76

Db 475 CTTTGACGACCACTTCTTGGCCGGGGGCTGACCTACTCGGCATCCGCTGGCGATGGC 416

QY 77 CTGCGGGTGGCGACGATCAACCGGATGGAAGACGAAGGATGGTGGCCAAACGCTGCCCG 136

Db 415 GCGGATGTGCGCCACCATCGACCGGATGAAGAGGAGATGTGTTGAGAACCGCGCCTC 356

QY 137 CATCGGCGACGAGTGTGCGACCGGGTCTGCGCGATCTGCGCGCCCGGACCGTTTCGGT 196

Db 355 TATCGGCAACGAGGTGTGCGCCCGGTCTCGAGGCGCTGGCGGAGGACGCGCATTTAT 296

QY 197 CGGCGAAGTCCGCGGCTCGGGCTCTTCTGGGCG 230

Db 295 CGGCGAGGTGCGGGTCCGGGCTGTTCAGGCG 262

RESULT 15

ABD00219

ID ABD00219 standard; DNA; 1371 BP.

XX ABD00219;

XX 29-JUL-2004 (first entry)

XX Klebsiella pneumoniae polynucleotide seqid 5994.

XX Recombinant expression vector; transcription regulatory element;

XX Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.

XX Klebsiella pneumoniae.

XX US6610836-B1.

XX 26-AUG-2003.

XX 27-JAN-2000; 2000US-00489039.

XX 29-JAN-1999; 99US-0117747P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton GL, Osborne M;

XX WPI; 2003-895346/82.

XX P-PSDB; ABO66648.

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.

XX Disclosure; SEQ ID NO 5994; 932pp; English.

XX The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae polypeptide of the invention

XX Sequence 1371 BP; 245 A; 409 C; 462 G; 255 T; 0 U; 0 Other;

Query Match 5.8%; Score 95.6; DB 11; Length 1371;

Best Local Similarity 65.4%; Pred. No. 1.4e-08;

Matches 140; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 17 CTTGCGGACCGGGCTACCGGGTGGCTGACGTACTCGGCATCCGCTGGCGACCGC 76

Db 942 CTTTGACGACCACTTCTTGGCCGGGGGCTGACCTACTCGGCATCCGCTGGCGATGGC 1001

QY 77 CTGCGGGTGGCGACGATCAACCGGATGGAAGACGAAGGATGGTGGCCAAACGCTGCCCG 136

Db 1002 GCGGATGTGCGCCACCATCGACCGGATGAAGAGGAGATGTGTTGAGAACCGCGCCTC 1061

QY 137 CATCGGCGACGAGTGTGCGACCGGGTCTGCGCGATCTGCGCGCCCGGACCGTTTCGGT 196

Db 1062 TATCGGCAACGAGGTGTGCGCCCGGTCTCGAGGCGCTGGCGGAGGACGCGCATTTAT 1121

QY 197 CGGCGAAGTCCGCGGCTCGGGCTCTTCTGGGCG 230

Db 1122 CGGCGAGGTGCGGGTCCGGGCTGTTCAGGCG 1155

Search completed: October 6, 2005, 20:46:31

Job time : 868 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 19:16:22 ; Search time 4974 Seconds  
(without alignments)  
12665.132 Million cell updates/sec

Title: US-10-607-752-115

Perfect score: 1655

Sequence: 1 gatctactactgaccttc.....atccaccatcaccatcactga 1655

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hcc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_g881.\*  
9: gb\_g882.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87.6	5.3	1798	9 AG171124	AG171124 Pan trogl
2	78.8	4.8	1772	9 CL508812	CL508812 SAIL_802
3	78	4.7	1516	4 BG809984	BG809984 mgct002xd
4	78	4.7	2332	9 AG363333	AG363333 Mus muscu
5	77.8	4.7	1173	6 CB207639	CB207639 AGENCOURT
6	76.8	4.6	2243	9 AG381986	AG381986 Mus muscu
7	76.4	4.6	1538	9 AG030607	AG030607 Pan trogl
8	76.4	4.6	1669	9 AG072737	AG072737 Pan trogl
9	76.4	4.6	1821	9 CL090560	CL090560 ISB1-17N1
10	75.8	4.6	1569	9 AG341503	AG341503 Mus muscu
11	75.6	4.6	925	9 CNS0091P	AL053013 Drosophil
12	75.6	4.6	1299	9 AG039481	AG039481 Pan trogl
13	75.4	4.6	1247	9 AG035314	AG035314 Pan trogl
14	74.8	4.5	1878	9 AG393083	AG393083 Mus muscu
15	73.4	4.4	1569	9 AG341503	AG341503 Mus muscu
16	73.2	4.4	937	9 AG080291	AG080291 Pan trogl
17	73	4.4	925	9 CNS0091P	AL053013 Drosophil
18	72.8	4.4	932	9 CNS0072Q	AL066742 Drosophil
19	72.8	4.4	1516	4 BG809984	BG809984 mgct002xd
20	72.6	4.4	940	7 CK404835	CK404835 AUF Ifsfn
21	72.6	4.4	2243	9 AG381986	AG381986 Mus muscu
22	72.4	4.4	1328	9 AG043615	AG043615 Pan trogl
23	71.4	4.3	1045	5 BUI190119	BUI190119 AGENCOURT
24	71.2	4.3	992	9 AG057280	AG057280 Pan trogl

25	71.2	4.3	1821	9 CL090560	CL090560 ISB1-17N1
26	71	4.3	1552	9 AG430101	AG430101 Mus muscu
27	71	4.3	1798	9 AG171124	AG171124 Pan trogl
28	70.8	4.3	932	9 CNS0072Q	AL066742 Drosophil
29	70.8	4.3	1406	9 CG756569	CG756569 P051-4-B0
30	70.4	4.3	1780	9 AG448243	AG448243 Mus muscu
31	70.2	4.2	1421	8 BZ569488	BZ569488 pac82-164
32	70.2	4.2	1772	9 CL508812	CL508812 SAIL_802
33	69.4	4.2	1137	4 BG809979	BG809979 mgct002xd
34	69.4	4.2	1151	9 AG046212	AG046212 Pan trogl
35	69.4	4.2	1280	8 CL470317	CL470317 SAIL_140
36	69.4	4.2	1610	8 BZ569386	BZ569386 pac82-164
37	69.2	4.2	971	5 BQ961185	BQ961185 AGENCOURT
38	69.2	4.2	1233	6 CA975828	CA975828 AGENCOURT
39	69	4.2	997	9 AG057392	AG057392 Pan trogl
40	68.8	4.2	1610	8 BZ569386	BZ569386 pac82-164
41	68.4	4.1	1126	9 AG064051	AG064051 Pan trogl
42	68.4	4.1	1780	9 AG448243	AG448243 Mus muscu
43	68.4	4.1	1878	9 AG393083	AG393083 Mus muscu
44	68.4	4.1	1981	9 CL515231	CL515231 SAIL_898
45	68	4.1	784	9 AG060328	AG060328 Pan trogl

## ALIGNMENTS

RESULT 1  
AG171124/c  
LOCUS AG171124 Pan troglodytes DNA, clone: RP43-040F09.TJ, genomic survey  
DEFINITION AG171124 1798 bp DNA linear GSS 09-JAN-2002  
sequence.  
ACCESSION AG171124 GI:16700802  
VERSION AG171124.1  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE 1  
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE BAC end sequences of Library RPCI-43  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1798)  
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43 This BAC  
end was generated during the R&D process and may have higher chance  
of PRIMER tracking errors.  
PRIMERS  
Sequencing: TJ  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI  
Location/Qualifiers  
1..1798  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-040F09.TJ"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 5.3%; Score 87.6; DB 9; Length 1798;

Best Local Similarity 41.1%; Pred. No. 1.1e-08; Matches 533; Conservative 0; Mismatches 750; Indels 13; Gaps 7;		
QY	21	GCGGACCGGCGTACCCGGGTGCTGAGCTACTCCGGGCATCCGTGGCGACCGCCTGC 80
Db	1691	GCGGCGGNGGCG 1632
QY	81	GCGGTGCGGACGATCAACCGGATGGAAGACGAAGGATGTTGGCC-AACTGTCGCCGAT 139
Db	1631	GCGGNNCG 1572
QY	140	CGGCGAGCAGGTCTCGACCGGCTCTGCGCATCTCGCGCGCGCGCGCGCGCGCGCG 197
Db	1571	CGGCG 1512
QY	198	GCGGAAGTCCGCGCGCTCGCGCTCTCTGCGCGCGGATCTGATCAGAAAGCGGCGCGTCTG 257
Db	1511	GNNGCGGCGCGGNGGCG 1452
QY	258	CGGTTGAGTCTCTCGGTGCCAGTGCCTGTCGACGAGCGTCTCTCGCGCGTGTGATGCG 317
Db	1451	CGGNGCG 1392
QY	318	GCGCGGTAGGCTCTCTCGTCCACACGTCACACGTCACGCGCGCGCGCGCGCGCGCG 377
Db	1391	CGNCG 1332
QY	378	AGTTCCGCGCTGTCGCGACCGCGCGAGGCGACGATTTCCGCTCCGCGGTGCGATCGGG 437
Db	1331	CG 1273
QY	438	TTGCGTCCGTCGCGCGACGACACAGCATCCACCGAGTGTGAGAGCAACGGTCTCCCGACG 497
Db	1272	NGCG 1213
QY	498	GTCCACATCTCCAGTCGATGACGC-CGCGAGCTCGGGAGCTTCGCGCGCGCGAGCAGCAC 556
Db	1212	CGGCG 1153
QY	557	GTGTTTTCAGATGCGCGTGCATGATCCCGGGTTCGCGCGCTGCTCGGGCTGCGCGA 616
Db	1152	NGCGGNGCG 1093
QY	617	GTCAGCAGTCCGCGAGGACATGACCGAGCGGAGAGCATCGGGCGCGGGATCTGATCA 676
Db	1092	GNNGCG 1034
QY	677	GCTCGGGAGCGCGGTCCCGACGACCGCAGCGTGGGAGCACCGAGACCGCGCGATGT 736
Db	1033	CG 974
QY	737	GCCCGCGCAGCAGCGCCAGCGTGCACCCCGCGGAGCGGGCCCGCGACCGCGTCGG 796
Db	973	CGCGCGNGGCG 914
QY	797	AGTCGACCCCG 856
Db	913	NNCG 854
QY	857	TCGCGAGCATCAGAACAGTAAAGCGGTTCGCGTTGATCAATGCTGTGTCAGCAGG 916
Db	853	CG 794
QY	917	CATCCGATGCGGAACACGACGACGCGAGCAGTCGCAAA---TCTGTCTCGCGACCTTGGC 973
Db	793	CGGCG 734
QY	974	GTCAGCGCGCGTCTGTGCTCCGMAACCGCGCGGAGTGTGCGCGCGCGCGCGCGCG 1029
Db	733	CG 674
QY	1030	CGGCTCTCTCATGCGCGTGTGTTAGTCTGCTCGTCTCGGTGGTGTCTTCGGAACGGGCC 1089

Db	673	CGGCG 614
QY	1090	CGCGCGCGCGTGTCTGTCGATACGGGATCTATCAGGAGTAGCGCGTCCAGCGGTAC 1149
Db	613	CG 554
QY	1150	TCTTCCGCGCGAGAACAGCGGTGCTCGCGCGCGAGACAGCGGTCTTCCGCGCAGATAC 1209
Db	553	CGGCG 494
QY	1210	ACCCAGCGGTGCGCGCGCATGTCCAGATCGTGGCGCGCGCGCGCGCGCGCGCGCG 1269
Db	493	CG 434
QY	1270	GATCTATCTGCGCGGTGTGTCGCGGAGAGGACGAGGCGCG 1305
Db	433	CGGCG 398
RESULT 2		
CL508812/c		
LOCUS		
DEFINITION		
SAIL 802_H02.v1 SAIL Collection Arabidopsis thaliana genomic clone		
SAIL_802_H02.v1, genomic survey sequence.		
CL508812.1 GI:46006132		
GSS.		
Arabidopsis thaliana (thale cress)		
Arabidopsis thaliana		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.		
1 (bases 1 to 1772)		
Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,		
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,		
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,		
Mittel,T., Katagiri,P., Glazebrook,J., Law,M. and Goff,S.A.		
A high-throughput Arabidopsis reverse genetics system		
Plant Cell 14 (12), 2985-2994 (2002)		
22356987		
PUBMED		
12468722		
COMMENT		
Contact: Sessions A		
Applied Trait Genetics		
Syngenta Biotechnology Inc.		
3054 Cornwalls Rd., Research Triangle Park, NC 27709, USA		
Email: allen.sessions@syngenta.com		
ABRC Stock Number CS835878; T-DNA left border flanking sequences of		
Syngenta Arabidopsis Insertion Library (SAIL) lines are available		
through the Arabidopsis Biological Resource Center (ABRC).		
Sequences represent a pool of amplified genomic regions and not		
single contiguous sequences.		
Class: TDNA tagged.		
FEATURES		
source		
1..1772		
/organism="Arabidopsis thaliana"		
/mol_type="genomic DNA"		
/ecotype="Columbia"		
/db_xref="taxon:3702"		
/clone_lib="SAIL 802_H02.v1"		
/clone_lib="SAIL Collection"		
/note="T-DNA left border sequences were isolated using a		
modified TAIL-PCR strategy"		
ORIGIN		
Query Match 4.8%; Score 78.8; DB 9; Length 1772;		
Best Local Similarity 44.0%; Pred. No. 9.4e-07;		
Matches 532; Conservative 0; Mismatches 669; Indels 9; Gaps 5;		
QY	64	CGTGGCGGACCGCTCGCGGTGCGGACGATCAACCGGATGAGAGGAGGCGATGTTGG 123
Db	1273	CG 1214
QY	124	CCAAACGTCGCGCGCATCGGCGAGGAGTGTCTCGGACCGGGTCTTGTGCGGATCTCGCGCGCC 183

```
Db      1213  CCGCCCGAGCGGGCGGCGGCGACCCCGGCGGGCGCGCCCGCGGTCGGAGCGTCC 1154
Qy      184  GGCACCGTTTCGGTCGGCGAAGTCGGCGGCTCGCGGCTCTTCTGGCGGGGATCTGATCCAG 243
Db      1153  GCGCGGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1094
Qy      244  AAGCGGCGGTCGTGCGGTTGAGTCTCTCGTGTCCAGTCCGCTCGACGCGGAGTCTGTTCG 303
Db      1093  GCGCGGGGCGGCGGCGCGCGCGAG-CGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1035
Qy      304  GCGCTGTGTATGCGCGCGCGCGGTAGCGTCTCTCGTCCACAGCTCAGCAACGCTGCCGGG 363
Db      1034  CCGCGCGGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 975
Qy      364  CGGATGATCTATAGTTTGGCTCTGTGCGCGAGCCCGCGGAGGCGAGCAGTTCGCTC 423
Db      974  C-----GCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 919
Qy      424  CGCGTCGATCGGGTTCGGTTCGGTCCGTCGCGCGCAGCACACAGCATCCACCGAGTTCGAGCA 483
Db      918  CGGCGCGCGTCCCGCGGGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 859
Qy      484  ACGGCTCCCGAGCGGTGCACATCTCCAGTTCGATGAACGC-CGCGAGCTCGGGGAGCGTCG 542
Db      858  CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 799
Qy      543  CCGCGCAGCAGCAGCTGTTGTCAGATGCGAGTGGCGCGGTGATGATCCCGGTTTCGGGTGCG 602
Db      798  CCGCGCGCGGCGTCTGCTCTTCGNGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 739
Qy      603  TCGGGCTCGCGGAGTCCAGCAGTCCGCGGAGCAGATGCACCGAGCGGAGCAGTCCGGC 662
Db      738  GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 679
Qy      663  GCGGGATCTGATCAGCTCGGGAGACCGCGGTGCGCGAGCAACCGCAGCTCGGGAAGCA--CC 720
Db      678  CCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 619
Qy      721  GAGACCGCGCGGATGTGCGCGCGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db      618  GCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 559
Qy      781  CCGCGGACCGGTTCGAGTCCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db      558  TCNGGCGCTGTTCGNGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 499
Qy      841  CACGGATGATCTGATCGGCGGCGATCAGAAAGCGGTGTTCCGGTTGAATCCA 900
Db      498  CGCCCCCTCGCGCGCGCGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 439
Qy      901  ATGTGCTGTAGCAGGATCCGATGCGGAAACACGACGACGCGAGCAGTTCGATCTGTCT 960
Db      438  GCGGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 379
Qy      961  TCGCGACCTCGGTCTAGCGGCGTCTGTGTCGCGCAACCGCGCGCGCGCGCGCGCGCGCG 1020
Db      378  GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 319
Qy      1021  CCGCTGCGCGCGCGCTCTCAAGCGGTTCTGTTCACTCGCTCGCTCGCTGCTGTTCTGTC 1080
Db      318  GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 259
Qy      1081  GAACGGGCGCGCGCGCGCGCGTCCGTCCGATACGG-GATCTATCAACGAGTGAAGCGGT 1139
Db      258  CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 199
Qy      1140  CCAGCGGATCTCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1199
Db      198  CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 139
Qy      1200  CGCCAGATACACCCAGCGGTGCGCGGCACTGTCAGATCGTGGGCGAGCGCGCGCGCGCG 1259
```

```
Db      138  CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 79
Qy      1260  GTGGAGATCG 1269
Db      78  CCGCGGATCG 69

RESULT 3
BG809984/c
LOCUS      1516 bp mRNA linear EST 22-MAY-2001
DEFINITION mgct002xdlif Magnaporthe grisea Appressorium Stage cDNA Magnaporthe
            grisea cDNA clone mgct002xdlif 5', mRNA sequence.
ACCESSION  BG809984
VERSION     BG809984.1 GI:14180964
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM    Magnaporthe grisea
REFERENCE   1 (bases 1 to 1516)
AUTHORS     Choi,W. and Dean,R.A.
TITLE       Construction and sequence analysis of an appressorium stage cDNA
            library in the rice blast fungus, Magnaporthe grisea
JOURNAL     Unpublished (2001)
COMMENT     Contact: Ralph A. Dean
            Fungal Genomics Laboratory
            North Carolina State University
            Campus Box 7251, Raleigh, NC 27695, USA
            Tel: 919-513-0020
            Fax: 919-513-0024
            Email: ralph_dean@ncsu.edu
            Seq primer: T3 primer (AATTAAACCTCACTAAAGG) .
            Location/Qualifiers
                1..1516
                /organism="Magnaporthe grisea"
                /mol_type="mRNA"
                /strain="70-15"
                /db_xref="taxon:148305"
                /clone="mgct002xdlif"
                /dev_stage="Germinated conidia on appressorium-inductive
                surface"
                /clone_lib="Magnaporthe grisea Appressorium Stage cDNA"
                /note="Vector: pBluescript SK(+) Vector; Site 1: BclRI;
                Site 2: XhoI; The appressorium formation-specific cDNA
                library was constructed from conidia germinated for 5-8 hr
                on an inductive surface. The library contains over 55,000
                clones with average insert size of 1.5 kbp."
```

## ORIGIN

```
Query Match      4.7%; Score 78; DB 4; Length 1516;
Best Local Similarity 41.6%; Pred. No. 1.4e-06;
Matches 486; Conservative 0; Mismatches 676; Indels 5; Gaps 4;

Qy      143  CGAGCAGGTCTCGGACCGGTCGCGGATCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 202
Db      1472  CGCGCGCGGNGCGGNGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1413
Qy      203  AGTCGCGGCTCGGCGTCTTCTGGCGGGATCTGATCAGAACGGGC-CGGTCTCGGG 261
Db      1412  GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1353
Qy      262  TTCAGGTCTCTCGTGCCAGTCCGTCGACGCGACGTCGTCGCGGCTGCTGATGCGGCG 321
Db      1352  GCGGCGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1293
Qy      322  CCGTAGCGCTCTCGGTCCACAGCGTCAGCACCGTGTCCCGCGGCGGATGGAATCATGTT 381
Db      1292  CGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1233
Qy      382  CGGCGCTGTGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 441
Db      1232  CNGTGGCGCGGTTCTCTCGCGCGGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1173
```









SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
1  
REFERENCE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
AUTHORS Totoki, Y., Watanabe, H. and Sakaki, Y.  
TITLE BAC end sequences of Library PTB  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1669)  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
[E-mail: chimpes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170]  
Clones are derived from the chimpanzee BAC library PTB. This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: -21M13  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
1. .1669  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-064F05.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"  
ORIGIN  
Query Match 4.6%; Score 76.4; DB 9; Length 1669;  
Best Local Similarity 42.9%; Pred. No. 3.2e-06;  
Matches 265; Conservative 0; Mismatches 346; Indels 7; Gaps 4;  
QY 419 CGTCCGGCTCGATCGGTTGGTTCGTCGGCCAGCACACCGATCCACCGAGGTC 478  
875 CG 816  
479 GAGCAACGGGTCCCGACGGTGACATCTCCAGTCGATGAACCGCGCGAGTCGCGGAC 538  
815 GTCNGGCTTTCG 756  
539 GTCGCGCGCGCAGCAGCATGTTTCAGATGCGCAGTCGCGTCGATGATCCCGGGTTCCGC 598  
755 GTTTGCG 697  
599 GTGTCG 658  
696 CCNCG 637  
659 GGGCGCGCGGATCTGATCAGCTCGGGGAGCGGGTGCACCAACCGCGCTGGGAAGCA 718  
636 GGGCG 577  
719 CCGAGACCGGCGCGATGTGCGCGCGCAGCAGCGCGCGCGCGCGCGCGCGCGCG 778  
576 CNGCG 519  
779 CCG 838  
518 CGGCG 459  
839 GCCACGGGATGGATCTGATCGGC---AGGCATCACGAACAGTAAGCGGTGTCGGTTGA 895  
458 GNNNNNCGNCG 399

QY 896 ATCCAATGTCTGTACGACGCGATCCGATCGCGAACACCGACCGCAGCGAGTCGCAAT 955  
398 GNNNGCGCGGNNNGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 339  
956 CTGT-CTCGCGACCTCGCGTCACGCGCGCTCGTGGTTCGCGAAACCGCGCGCGATGCG 1014  
338 CCGGCG 279  
1015 CGCGCGCGCGCTCGCGCGCG 1032  
278 CGCGGCGCGCGCGCGCGCG 261  
RESULT 9  
CL090560/c  
LOCUS  
DEFINITION  
CL090560  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Xenopus tropicalis (western clawed frog)  
Xenopus tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Silurana.  
1 (bases 1 to 1821)  
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,  
Mardis, E. and Wilson, R.  
A physical map of the xenopus tropicalis genome  
Unpublished (2003)  
Contact: Richard K Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@wustl.edu  
Insert Length: 75000 Std Error: 0.00  
Seq primer: T7 TAATACGACTCACTATAGG  
Class: BAC ends  
High quality sequence start: 591  
High quality sequence stop: 665.  
High quality sequence stop: 665.  
Location/Qualifiers  
1. .1821  
/organism="Xenopus tropicalis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:8364"  
/clone="ISB1-17N15"  
/clone\_lib="ISB1"  
/note="Vector: pBelOBAC11; ISB-1 Xenopus tropicalis BAC  
Library Segment 1"  
ORIGIN  
Query Match 4.6%; Score 76.4; DB 9; Length 1821;  
Best Local Similarity 44.2%; Pred. No. 3.2e-06;  
Matches 491; Conservative 0; Mismatches 611; Indels 8; Gaps 4;  
QY 207 CGCGCGCTCGGCGTCTTCTGGCGCGGATCTGATCCAGACGGCGCGCTCGCGGTTGAG 266  
1758 CG 1699  
267 GTCTCTCGGTCCAGTCGATCGACGTCGTCGCGCGCTGCTGATCGCGCGCGCGTA 326  
1698 CGGCG 1639  
327 GCGGTCTCTCGGTCCACACGTCAGACCGTGCCTCGCGCGCGCGATGATCTATCAGTTGGCC 386  
1638 CAGCG 1579  
387 CTGCTCG 446  
1578 GGGCG 1519  
447 TCGCGCGCAGCACACCGATCCACCGCGAGGTCCAGCAACGGGTCCCGGACGTTGCATC 506







[illegible][illegible]



Fr1 Oct 7 10:27:10 2005

[illegible]

Search completed: October 7, 2005, 00:06:41  
Job time : 4983 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 6, 2005, 20:14:37 ; Search time 1112 Seconds  
(without alignments)  
10365.839 Million cell updates/sec

Title: US-10-607-752-115  
Perfect score: 1655  
Sequence: 1 gatcatcactcagcttc.....atcaccatcaccatcactga 1655

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues  
Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1655	100.0	1655	18	US-10-607-752-115
2	1655	100.0	1749	18	US-10-607-752-115
3	1655	100.0	1749	18	US-10-607-752-115
4	1623	98.1	1623	14	US-10-607-752-89
5	1623	98.1	1623	18	US-10-607-752-89
6	1413	85.4	1413	14	US-10-607-752-88
7	1413	85.4	1413	18	US-10-607-752-88

8	1247	75.3	1263	14	US-10-100-679-87	Sequence 87, Appl
9	1247	75.3	1263	18	US-10-607-752-87	Sequence 87, Appl
10	1116	67.4	1116	14	US-10-100-679-86	Sequence 86, Appl
11	1116	67.4	1116	18	US-10-607-752-86	Sequence 86, Appl
12	1011.4	61.1	1749	14	US-10-100-679-56	Sequence 56, Appl
13	1011.4	61.1	1749	18	US-10-607-752-56	Sequence 56, Appl
14	843	50.9	843	14	US-10-100-679-85	Sequence 85, Appl
15	843	50.9	843	18	US-10-607-752-85	Sequence 85, Appl
16	740.2	44.7	1749	14	US-10-100-679-57	Sequence 57, Appl
17	740.2	44.7	1749	18	US-10-607-752-57	Sequence 57, Appl
18	660	39.9	660	14	US-10-100-679-84	Sequence 84, Appl
19	660	39.9	660	18	US-10-607-752-84	Sequence 84, Appl
20	363	21.9	363	14	US-10-100-679-83	Sequence 83, Appl
21	363	21.9	363	18	US-10-607-752-83	Sequence 83, Appl
22	291	17.6	291	14	US-10-100-679-15	Sequence 15, Appl
23	291	17.6	291	18	US-10-607-752-15	Sequence 15, Appl
24	261	15.8	261	14	US-10-100-679-18	Sequence 18, Appl
25	261	15.8	261	18	US-10-607-752-18	Sequence 18, Appl
26	226	13.7	697	14	US-10-100-679-14	Sequence 14, Appl
27	226	13.7	697	18	US-10-607-752-14	Sequence 14, Appl
28	225	13.6	225	14	US-10-100-679-82	Sequence 82, Appl
29	225	13.6	225	18	US-10-607-752-82	Sequence 82, Appl
30	210	12.7	210	14	US-10-100-679-13	Sequence 13, Appl
31	210	12.7	210	18	US-10-607-752-13	Sequence 13, Appl
32	177	10.7	177	14	US-10-100-679-21	Sequence 21, Appl
33	177	10.7	177	18	US-10-607-752-21	Sequence 21, Appl
34	147	8.9	147	14	US-10-100-679-16	Sequence 16, Appl
35	147	8.9	147	18	US-10-607-752-16	Sequence 16, Appl
36	138	8.3	138	14	US-10-100-679-17	Sequence 17, Appl
37	138	8.3	138	18	US-10-607-752-17	Sequence 17, Appl
38	132.4	8.0	1353	15	US-10-156-761-4535	Sequence 4535, Ap
39	132.4	8.0	9025608	15	US-10-156-761-4535	Sequence 1, Appl
40	132	8.0	132	14	US-10-100-679-20	Sequence 20, Appl
41	132	8.0	132	18	US-10-607-752-20	Sequence 20, Appl
42	114	6.9	114	14	US-10-100-679-11	Sequence 11, Appl
43	114	6.9	114	18	US-10-607-752-11	Sequence 11, Appl
44	96	5.8	96	14	US-10-100-679-9	Sequence 9, Appl
45	96	5.8	96	18	US-10-607-752-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1  
US-10-607-752-115  
; Sequence 115, Application US/10607752  
; Publication No. US20040072224A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder  
; TITLE OF INVENTION: and Methods for Their Use  
; FILE REFERENCE: 11000.1042C3  
; CURRENT APPLICATION NUMBER: US/10/607,752  
; CURRENT FILING DATE: 2003-06-26  
; PRIOR APPLICATION NUMBER: 10/100,679  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/351,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 115  
; LENGTH: 1655  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-10-607-752-115

Query Match 100.0%; Score 1655; DB 18; Length 1655;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCTATCTACTGACCTTGC CGACCGGGCGTACCGGGTGGCTTGACGTACTCCGGCC 60  
DB |||||  
1 GATCTATCTACTGACCTTGC CGACCGGGCGTACCGGGTGGCTTGACGTACTCCGGCC 60  
QY 61 ATCCGCTGGCGACCGCTTGC CGGCTCGACACGATCAACGCGATGGAAGACGAAGGCATGG 120  
DB |||||  
61 ATCCGCTGGCGACCGCTTGC CGGCTCGACACGATCAACGCGATGGAAGACGAAGGCATGG 120  
QY 121 TGGCCAAACGTGCTCCGCGATCGGCGAGCAGGTGCTCGGACCGGGTCTTGCGGATCTCGCCG 180  
DB |||||  
121 TGGCCAAACGTGCTCCGCGATCGGCGAGCAGGTGCTCGGACCGGGTCTTGCGGATCTCGCCG 180  
QY 181 CCGGCGACCTTGCCTCGGCGAAGTCCGCGGCTCGGCGTCTTCTGGGCGGATCTGATC 240  
DB |||||  
181 CCGGCGACCTTGCCTCGGCGAAGTCCGCGGCTCGGCGTCTTCTGGGCGGATCTGATC 240  
241 CAGAACGGGCGGCTTGC CGGCTTGAAGTCTCGTGC CCAAGTCCGCTCGACGCGACGTCCG 300  
DB |||||  
241 CAGAACGGGCGGCTTGC CGGCTTGAAGTCTCGTGC CCAAGTCCGCTCGACGCGACGTCCG 300  
QY 301 TCGGCGCTGGTGTAGTCGGCGCGCGTGGGTCCTCGGTC CCAACGTCAGCAACCGTGC 360  
DB |||||  
301 TCGGCGCTGGTGTAGTCGGCGCGCGTGGGTCCTCGGTC CCAACGTCAGCAACCGTGC 360  
QY 361 GGGCGGATGATCTATCAGTTCCGCGCTTGTGTC CCGACGCGCGCGGCGAGCCAGTTCCG 420  
DB |||||  
361 GGGCGGATGATCTATCAGTTCCGCGCTTGTGTC CCGACGCGCGCGGCGAGCCAGTTCCG 420  
QY 421 CTCGGGCTCGATCGGCTTGGCTCCGTC CGGCGCAGACACACGATCCACCGCGAGTCCGA 480  
DB |||||  
421 CTCGGGCTCGATCGGCTTGGCTCCGTC CGGCGCAGACACACGATCCACCGCGAGTCCGA 480  
QY 481 GCAACGGGCTCCCGACGGTGCA CATCTCCAGTGCATGAAACGCGGAGCTCGGGGACGT 540  
DB |||||  
481 GCAACGGGCTCCCGACGGTGCA CATCTCCAGTGCATGAAACGCGGAGCTCGGGGACGT 540  
QY 541 CGGGCGCAGCAGCAGCTTGTTCAGATGGCAGTTCGCGCTGCATGATCCGCGGTTCCGCGT 600  
DB |||||  
541 CGGGCGCAGCAGCAGCTTGTTCAGATGGCAGTTCGCGCTGCATGATCCGCGGTTCCGCGT 600  
QY 601 CGTCCGGCTCGCGAGTCCAGCGAGTCCGCGCGACATCGACCGACCGGAAACGACTCCG 660  
DB |||||  
601 CGTCCGGCTCGCGAGTCCAGCGAGTCCGCGCGACATCGACCGACCGGAAACGACTCCG 660  
QY 661 CGCGGGATCTGATCAGCTCGGGAGCCGGGTGCCCAGCAACGCGTGGGAAGCACC 720  
DB |||||  
661 CGCGGGATCTGATCAGCTCGGGAGCCGGGTGCCCAGCAACGCGTGGGAAGCACC 720  
QY 721 GAGACCGCGCGATGTGCTCCGCGCAGCAGCGCCCGCTGCACCCCGCGGGACCGGGCC 780  
DB |||||  
721 GAGACCGCGCGATGTGCTCCGCGCAGCAGCGCCCGCTGCACCCCGCGGGACCGGGCC 780  
QY 781 CCGCGGACCGGCTCGGAGTGCACCCCGCGCGCCACCGCGCGCGTGGTTCAGCATCAGC 840  
DB |||||  
781 CCGCGGACCGGCTCGGAGTGCACCCCGCGCGCCACCGCGCGCGTGGTTCAGCATCAGC 840  
QY 841 CACGGGATGATCTGATCGGCGAGCATCA CAAACAGTAAGCGGTTCGGGTTGAATCCA 900  
DB |||||  
841 CACGGGATGATCTGATCGGCGAGCATCA CAAACAGTAAGCGGTTCGGGTTGAATCCA 900  
QY 901 ATGTGCTGTACGAGGATCCGATGCGGAACACCGACCGCAGCAGTCCGCAATCTGTC 960  
DB |||||  
901 ATGTGCTGTACGAGGATCCGATGCGGAACACCGACCGCAGCAGTCCGCAATCTGTC 960  
QY 961 TCGCGACCGCTCGCGCGCTCGTGGCTCGCGCAACCGCGCGGATGTTCGCGCGC 1020  
DB |||||  
961 TCGCGACCGCTCGCGCGCTCGTGGCTCGCGCAACCGCGCGGATGTTCGCGCGC 1020  
QY 1021 CCGTTCGGCGCGCTCTCCATGGCGGTTCCGTCAGTCCGTCGTCGCGGTCGTTTCG 1080  
DB |||||  
1021 CCGTTCGGCGCGCTCTCCATGGCGGTTCCGTCAGTCCGTCGTCGCGGTCGTTTCG 1080

QY 1081 GAACGGGCCCGCGCGCTCGTCCGTCAGGATCTATCAGCAGGTAGGCCGTC 1140  
DB |||||  
1081 GAACGGGCCCGCGCGCTCGTCCGTCAGGATCTATCAGCAGGTAGGCCGTC 1140  
QY 1141 CAGCGGTACTTTCGCCCCAGAAACAGCGGTGCGCGCGCAGACAGCGGTCTCTGCC 1200  
DB |||||  
1141 CAGCGGTACTTTCGCCCCAGAAACAGCGGTGCGCGCGCAGACAGCGGTCTCTGCC 1200  
QY 1201 GCCAGATACACCCAGGCGGTGCGGCATGTCAGATCGTGCCAGCGCGCGCACGG 1260  
DB |||||  
1201 GCCAGATACACCCAGGCGGTGCGGCATGTCAGATCGTGCCAGCGCGCGCACGG 1260  
QY 1261 TGGAGATCGGATCTATCGCGCGCTGTGCGGGAAGACAGGCCGTAGCGGCTTGCACT 1320  
DB |||||  
1261 TGGAGATCGGATCTATCGCGCGCTGTGCGGGAAGACAGGCCGTAGCGGCTTGCACT 1320  
QY 1321 AGGTCCGCGGTTGCGGAGAAAGAGACTACATCGACCGAGCTTGGCAACATCGGC 1380  
DB |||||  
1321 AGGTCCGCGGTTGCGGAGAAAGAGACTACATCGACCGAGCTTGGCAACATCGGC 1380  
QY 1381 CGTATCTGCCAGCTGAGGTTCCGCTCTCGTCCGATCTATCGCCGCGACCGCGCTGCG 1440  
DB |||||  
1381 CGTATCTGCCAGCTGAGGTTCCGCTCTCGTCCGATCTATCGCCGCGACCGCGCTGCG 1440  
QY 1441 CCGGCGACCGGTGAGTTCGTCAGTACCCGAACTCTTGAGAGCTTAAGGCCAATTGG 1500  
DB |||||  
1441 CCGGCGACCGGTGAGTTCGTCAGTACCCGAACTCTTGAGAGCTTAAGGCCAATTGG 1500  
QY 1501 AAGATCTTGGACCTTCCATCAATAGAGGAAAGCATCGCCCTAGGGATCCGTAGCG 1560  
DB |||||  
1501 AAGATCTTGGACCTTCCATCAATAGAGGAAAGCATCGCCCTAGGGATCCGTAGCG 1560  
QY 1561 GCCCGGTGTTTCAGTGAACTTGGCGAGGCAATCCATCGCGCGCAGCCCGCAGCGCG 1620  
DB |||||  
1561 GCCCGGTGTTTCAGTGAACTTGGCGAGGCAATCCATCGCGCGCAGCCCGCAGCGCG 1620  
QY 1621 AAATCCACGATCCCATCACCATCACCATCACTCACTGA 1655  
DB |||||  
1621 AAATCCACGATCCCATCACCATCACCATCACTCACTGA 1655

RESULT 2

US-10-100-679-58  
; Sequence 58, Application US/10100679  
; Publication No. US20030054013A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder.  
; FILE REFERENCE: 11000.1042C2  
; CURRENT APPLICATION NUMBER: US/10/100,679  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/351,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58  
; LENGTH: 1749  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-10-100-679-58

Query Match 100.0%; Score 1655; DB 14; Length 1749;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCTATCTACTGACCTTGC CGCAGCGGGGTGACCGGGTGGCTTGACGTACTCCGGCC 60

Db 95 GATCTATCTACTCGA CTTTCGCCGACCGGCGGTACCGGGTGGCTGAGTACTCTCGGCC 154  
 Qy 61 ATCCGCTGGCGAACCGCTTCGCGGGTTCGCGACATCAACCGCGATGGAAGACGAAGGATGG 120  
 Db 155 ATCCGCTGGCGAACCGCTTCGCGGGTTCGCGACATCAACCGCGATGGAAGACGAAGGATGG 214  
 Qy 121 TGGCCAAACGCTGCCGATCCGCGACGAGCAGGTGCTCCGACCGGGTCTGCGCGATCTCGCCG 180  
 Db 215 TGGCCAAACGCTGCCGATCCGCGAGCAGGTGCTCCGACCGGGTCTGCGCGATCTCGCCG 274  
 Qy 181 CCGGCAACCGCTTCGGTTCGGCGAAGTCCGCGGCTTCGCGCGTCTTCGCGCGGATCTGATC 240  
 Db 275 CCGGCAACCGCTTCGGTTCGGCGAAGTCCGCGGCTTCGCGCGTCTTCGCGCGGATCTGATC 334  
 Qy 241 CAGAAACGGGCGGCTTCGCGGGTTCGAGGTCTCCGTCGCGGATGCTCGCGGATCGAGCTCG 300  
 Db 335 CAGAAACGGGCGGCTTCGCGGGTTCGAGGTCTCCGTCGCGGATGCTCGCGGATCGAGCTCG 394  
 Qy 301 TCGGCGGTGATGATGCGGCGCGGCTAGGCGTCTCCGTCACACGTCACACGTCACACCGTCCG 360  
 Db 395 TCGGCGGTGATGATGCGGCGCGGCTAGGCGTCTCCGTCACACGTCACACGTCACACCGTCCG 454  
 Qy 361 GGGCGGATGATCTATCAGTTTCGGGCTTCGGTCGCGGCTTCGCGGCGGCGGCGGCGGCGGCTTCG 420  
 Db 455 GGGCGGATGATCTATCAGTTTCGGGCTTCGGTCGCGGCTTCGCGGCGGCGGCGGCGGCGGCTTCG 514  
 Qy 421 CTCGGCGTTCGATGCGGCTTCGGTTCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 480  
 Db 515 CTCGGCGTTCGATGCGGCTTCGGTTCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 574  
 Qy 481 GCAACGGGTCGCGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 540  
 Db 575 GCAACGGGTCGCGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 634  
 Qy 541 CGCGGCGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 600  
 Db 635 CGCGGCGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 694  
 Qy 601 CGTCGGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 660  
 Db 695 CGTCGGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 754  
 Qy 661 CGCGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 720  
 Db 755 CGCGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 814  
 Qy 721 GAGACCGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 780  
 Db 815 GAGACCGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 874  
 Qy 781 CCGCGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 840  
 Db 875 CCGCGGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 934  
 Qy 841 CACCGGATGATCTGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 900  
 Db 935 CACCGGATGATCTGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 994  
 Qy 901 ATGTGCTGTACGAGGATCGGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 960  
 Db 995 ATGTGCTGTACGAGGATCGGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 1054  
 Qy 961 TCGCGACCTTCGGGCTTCAGCGGCGGCTTCGGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 1020  
 Db 1055 TCGCGACCTTCGGGCTTCAGCGGCGGCTTCGGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCTTCG 1114  
 Qy 1021 CCGCTGCGGCGGCTTCAGCGGCGGCTTCGGTTCAGTGCCTTCGTCGCGGCGGCGGCGGCGGCTTCG 1080  
 Db 1115 CCGCTGCGGCGGCTTCAGCGGCGGCTTCGGTTCAGTGCCTTCGTCGCGGCGGCGGCGGCGGCTTCG 1174  
 Qy 1081 GAAACGGGCGGCGGCTTCAGCGGCGGCTTCGGTTCAGTGCCTTCGTCGCGGCGGCGGCGGCTTCG 1140

Db 1175 GAACGGGCGGCGGCGGCGGCTTCGTCGATACCGGATCTATACGAGGATAGGCGGCTC 1234  
 Qy 1141 CAGCGCTACTCTTCGCGCGGCGGCGGCTTCGTCGCGGCGGCGGCGGCGGCGGCTTCGCGC 1200  
 Db 1235 CAGCGCTACTCTTCGCGCGGCGGCGGCGGCTTCGTCGCGGCGGCGGCGGCGGCGGCTTCGCGC 1294  
 Qy 1201 GCCAGATACACCCAGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1260  
 Db 1295 GCCAGATACACCCAGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1354  
 Qy 1261 TGGAGATCGGATCTATCGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1320  
 Db 1355 TGGAGATCGGATCTATCGCGGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1414  
 Qy 1321 AGTTCGCGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1380  
 Db 1415 AGTTCGCGCGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1474  
 Qy 1381 CGTATCTGCAGCTGAGGTTCGCGGCTTCGTCGATCTATCGCGGCGGCGGCGGCGGCGGCGGCGG 1440  
 Db 1475 CGTATCTGCAGCTGAGGTTCGCGGCTTCGTCGATCTATCGCGGCGGCGGCGGCGGCGGCGGCGG 1534  
 Qy 1441 CCGGCGGCGGCGGCTTCGTCGATCTATCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1500  
 Db 1535 CCGGCGGCGGCGGCTTCGTCGATCTATCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1594  
 Qy 1501 AGATATCTGGACCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1560  
 Db 1595 AGATATCTGGACCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1654  
 Qy 1561 GCCCGGCTTCGAGTGAACTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1620  
 Db 1655 GCCCGGCTTCGAGTGAACTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1714  
 Qy 1621 AAATCCAGGATCCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 1655  
 Db 1715 AAATCCAGGATCCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 1749

RESULT 3

US-10-607-752-58  
 ; Sequence 58, Application US/10607752  
 ; Publication No. US2004007222A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Delcayre, Alain  
 ; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder  
 ; TITLE OF INVENTION: and Methods for Their Use  
 ; FILE REFERENCE: 11000.1042C3  
 ; CURRENT APPLICATION NUMBER: US/10/607,752  
 ; CURRENT FILING DATE: 2003-06-26  
 ; PRIOR APPLICATION NUMBER: 10/100,679  
 ; PRIOR FILING DATE: 2002-03-14  
 ; PRIOR APPLICATION NUMBER: 09/450,072  
 ; PRIOR FILING DATE: 1999-11-29  
 ; PRIOR APPLICATION NUMBER: 09/351,348  
 ; PRIOR FILING DATE: 1999-07-12  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 58  
 ; LENGTH: 1749  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Made in a lab  
 US-10-607-752-58

Query Match 100.0%; Score 1655; DB 18; Length 1749;  
 Best Local Similarity 100.0%; Pred.No. 0;  
 Matches 1655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GATCTATCTACTCGACCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60  
 Db 95 GATCTATCTACTCGACCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 154

QY 61 ATCCGCTGGCGACCGCTTGGCGGTGCGACGATCAACCGGATGGAAGCAAGCATGG 120  
DB 155 ATCCGCTGGCGACCGCTTGGCGGTGCGACGATCAACCGGATGGAAGCAAGCATGG 214  
QY 121 TGGCCAAACGTGCGCCGATCGGCGACAGGTGCTCGGACCGGGTCTGCGCGG 180  
DB 215 TGGCCAAACGTGCGCCGATCGGCGACAGGTGCTCGGA CGGGTCTGCGCGATCTCGCG 274  
QY 181 CCGCGACCGCTTGGGTGCGGAAAGTCCGCGGCTCGGGGCTTCTGGGCGGGATCTGATC 240  
DB 275 CCGCGACCGCTTGGGTGCGGAAAGTCCGCGGCTCGGGGCTTCTGGGCGGGATCTGATC 334  
QY 241 CAGAA CGGGCGGCTGCGGGTGGGTGAGGTCTCGGTGCGGCGGAGTCCGCGGAGGTGCG 300  
DB 335 CAGAA CGGGCGGCTGCGGGTGGGTGAGGTCTCGGTGCGGCGGAGTCCGCGGAGGTGCG 394  
301 TCGGCGCTGATGATCGGCGCGCGGTAGGGTCTCGGTCCACAACTCAGACACCGGTGCC 360  
DB 395 TCGGCGCTGATGATCGGCGCGCGGTAGGGTCTCGGTCCACAACTCAGACACCGGTGCC 454  
QY 361 GGGCGGATGATCTATGATGCGGCTTGGGTGAGGTCTCGGTGCGGCGGAGTCCGCGGAGGTGCG 420  
DB 455 GGGCGGATGATCTATGATGCGGCTTGGGTGAGGTCTCGGTGCGGCGGAGTCCGCGGAGGTGCG 514  
QY 421 CTCGGGCTGATGATCGGCGCGCGGTAGGGTCTCGGTCCACAACTCAGACACCGGTGCC 480  
DB 515 CTCGGGCTGATGATCGGCGCGCGGTAGGGTCTCGGTCCACAACTCAGACACCGGTGCC 574  
QY 481 GCAA CGGGTCCCCGACGCTGACATCTCCAGTTCGATGAACCGCGGAGCTCGGGGACGT 540  
DB 575 GCAA CGGGTCCCCGACGCTGACATCTCCAGTTCGATGAACCGCGGAGCTCGGGGACGT 634  
QY 541 CCGCGGCGACGACGACGCTTGGTTCAGATGCGAGTTCGCGGTGCGATGATCCCGGGTTCGGCGT 600  
DB 635 CCGCGGCGACGACGACGCTTGGTTCAGATGCGAGTTCGCGGTGCGATGATCCCGGGTTCGGCGT 694  
QY 601 CGTGCGGCTGCGCGGATTCAGCAGTTCGCGGAGCATGCAACCGCGGAGCATCGG 660  
DB 695 CGTGCGGCTGCGCGGATTCAGCAGTTCGCGGAGCATGCAACCGCGGAGCATCGG 754  
QY 661 GCGCGGATCTGATCAGTTCGCGGAGCGCGGCTGCCAGCAACCGCGGAGCATCGG 720  
DB 755 GCGCGGATCTGATCAGTTCGCGGAGCGCGGCTGCCAGCAACCGCGGAGCATCGG 814  
721 GAGACCGGCGGATGCTGCTCGCGGAGCGAGCGCGGCTGCCAGCAACCGCGGAGCATCGG 780  
DB 815 GAGACCGGCGGATGCTGCTCGCGGAGCGAGCGCGGCTGCCAGCAACCGCGGAGCATCGG 874  
QY 781 CCGCGGACCGGCTCGGAGTTCGACCCCGGCGGCGGCGGCGGCGGCTGCTGAGCATCAGC 840  
DB 875 CCGCGGACCGGCTCGGAGTTCGACCCCGGCGGCGGCGGCGGCGGCTGCTGAGCATCAGC 934  
QY 841 CAGCGGATGATCTGATTCGCGGAGCATTCAGAACTGAGCGGTGTTCCGGTTGAATCCA 900  
DB 935 CAGCGGATGATCTGATTCGCGGAGCATTCAGAACTGAGCGGTGTTCCGGTTGAATCCA 994  
QY 901 ATGTGCTGTGAGCAGGATCCGATGCGGAAACACCGACCGAGCAGTTCGCAATCTGTC 960  
DB 995 ATGTGCTGTGAGCAGGATCCGATGCGGAAACACCGACCGAGCAGTTCGCAATCTGTC 1054  
QY 961 TCGGACCGCTGGGTGACGCGGCGGTGCTGGCTCGGCAACCGCGGCGGATGTCGCGCGG 1020  
DB 1055 TCGGACCGCTGGGTGACGCGGCGGTGCTGGCTCGGCAACCGCGGCGGATGTCGCGCGG 1114  
QY 1021 CCGCTGCGGCGGCTCTTCAATGCGCGGTTCTGTTTCACTGCTGCTGCGGCTGCTGCTG 1080  
DB 1115 CCGCTGCGGCGGCTCTTCAATGCGCGGTTCTGTTTCACTGCTGCTGCGGCTGCTGCTG 1174  
QY 1081 GAACGGGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
DB 1175 GAACGGGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1234

QY 1141 CAGCCGTACTCTTTCGCCCCAGAAACAGCGGTGCTCGCGCGGCGACACAGCGGTCTCTGCC 1200  
DB 1235 CAGCCGTACTCTTTCGCCCCAGAAACAGCGGTGCTCGCGCGGCGACACAGCGGTCTCTGCC 1294  
QY 1201 GCCAGATACACCCAGCGGTGCGGATGTCAGATCTGTCAGCGCGGCGGCGGCGGCGGCGG 1260  
DB 1295 GCCAGATACACCCAGCGGTGCGGATGTCAGATCTGTCAGCGCGGCGGCGGCGGCGGCGG 1354  
QY 1261 TGGAGATCGGATCTATTCGCGGCTGTCGGGGAAGGACGAGCGCTAGCGGCTTTCGCACT 1320  
DB 1355 TGGAGATCGGATCTATTCGCGGCTGTCGGGGAAGGACGAGCGCTAGCGGCTTTCGCACT 1414  
QY 1321 AGCTCGCCCGGCTTGGCGAGAGCAGGACTATATCGACCGAGCTTTCGCGCAACATCGGCG 1380  
DB 1415 AGCTCGCCCGGCTTGGCGAGAGCAGGACTATATCGACCGAGCTTTCGCGCAACATCGGCG 1474  
QY 1381 CGTATCTGCCAGCTGAGGTTCGCTGTCGATCTATTCGCGCGGCGGCGGCGGCGGCGG 1440  
DB 1475 CGTATCTGCCAGCTGAGGTTCGCTGTCGATCTATTCGCGCGGCGGCGGCGGCGGCGG 1534  
QY 1441 CCGGCAACCGGTGAGTCTGTCAGTACCCGAAAGCTTTCGAGAGCTTAAGGCAATTCGG 1500  
DB 1535 CCGGCAACCGGTGAGTCTGTCAGTACCCGAAAGCTTTCGAGAGCTTAAGGCAATTCGG 1594  
QY 1501 AAGATACTTGACCTTCCCATCAATAGAGGAAAGCATCGCCTAGGGGATCCGTAGCGG 1560  
DB 1595 AAGATACTTGACCTTCCCATCAATAGAGGAAAGCATCGCCTAGGGGATCCGTAGCGG 1654  
QY 1561 GCCCGGTGTTTCAGTGAATTCGCGGAGGCGAATCCATCGCGCGGCGGCGGCGGCGG 1620  
DB 1655 GCCCGGTGTTTCAGTGAATTCGCGGAGGCGAATCCATCGCGCGGCGGCGGCGGCGG 1714  
QY 1621 AATCCAGGATCCCATCACCATCACCATCCTCTGAGAGCTTAAGGCAATTCGG 1655  
DB 1715 AATCCAGGATCCCATCACCATCACCATCCTCTGAGAGCTTAAGGCAATTCGG 1749

RESULT 4

US-10-100-679-89  
; Sequence 89, Application US/10100679  
; Publication No. US20030054013A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcavre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; TITLE OF INVENTION: and Methods for Their Use  
; FILE REFERENCE: 11000.1042c2  
; CURRENT APPLICATION NUMBER: US/10/100,679  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/351,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 89  
; LENGTH: 1623  
; TYPE: DNA  
; ORGANISM: Mycobacterium vaccae  
US-10-100-679-89

Query Match 98.1%; Score 1623; DB 14; Length 1623;  
Best Local Similarity 100.0%; Fred. No. 0;  
Matches 1623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 ATCTACTTCACCTTCCCGACCGGCGGTACCGGGTGGCTTACGCTACTCCGCGCCATCCG 65  
DB 1 ATCTACTTCACCTTCCCGACCGGCGGTACCGGGTGGCTTACGCTACTCCGCGCCATCCG 60  
QY 66 CTGGCGACCGCTGCGCGGTGCGGACGATCAACGCGATGGAAGCAAGGCAATGGTGGCC 125  
DB 61 CTGGCGACCGCTGCGCGGTGCGGACGATCAACGCGATGGAAGCAAGGCAATGGTGGCC 120



QY 186 CACCGTTCCGCGAAGTCCGCGGCTCTCGGGTCTTCTGGCGGGATCTGATCAGAA 245  
DB 181 CACCGTTCCGTCGCGAAGTCCGCGGCTCTCGGGTCTTCTGGCGGGATCTGATCAGAA 240  
QY 246 CGGGCCGGTCTGGGGTTGAGTCTCGGTGCCAGTCCGCTCGAGCGACGTCGTCGGC 305  
DB 241 CGGGCCGGTCTGGGGTTGAGTCTCGGTGCCAGTCCGCTCGAGCGACGTCGTCGGC 300  
QY 306 GCTGGTGATCGCGCCCGTAGCGTCTTGCTGCTCAACAGTCAAGCAGTCCCGGGCG 365  
DB 301 GCTGGTGATCGCGCCCGTAGCGTCTTGCTGCTCAACAGTCAAGCAGTCCCGGGCG 360  
QY 366 GATGGATCTATCAGTTTGGTCCGCTCGAGCGCCCGAGGGCAGCAGTTCGGTCCG 425  
DB 361 GATGGATCTATCAGTTTGGTCCGCTCGAGCGCCCGAGGGCAGCAGTTCGGTCCG 420  
QY 426 GCCTCGATCGGGTTGGTCCGCTCGAGCAGCAGCAGCAGTCCACCGAGGTCGAGCAAC 485  
DB 421 GCCTCGATCGGGTTGGTCCGCTCGAGCAGCAGCAGCAGTCCACCGAGGTCGAGCAAC 480  
QY 486 GGGTCCCGCAGCGTGACATCTCCAGTCCGATGAACGCGCGAGTCCGGGACGTCGCG 545  
DB 481 GGGTCCCGCAGCGTGACATCTCCAGTCCGATGAACGCGCGAGTCCGGGACGTCGCG 540  
QY 546 CGCAGACGACGTTGTTTCAGATGGCAGTCCGCTGATGATCCCGGGTTCGGGGTCTCG 605  
DB 541 CGCAGACGACGTTGTTTCAGATGGCAGTCCGCTGATGATCCCGGGTTCGGGGTCTCG 600  
QY 606 GGGTCCCGCAGTCCAGCGAGTCCGAGCAGCAGCAGCAGCAGCAGTCCGCGCGCG 665  
DB 601 GGGTCCCGCAGTCCAGCGAGTCCGAGCAGCAGCAGCAGCAGCAGTCCGCGCGCG 660  
QY 666 GGGTCTGATCAGTCCGGGAGCGGGTCCAGCAACGCGCGTCCGAGCAGCAGCAGCAG 725  
DB 661 GGGTCTGATCAGTCCGGGAGCGGGTCCAGCAACGCGCGTCCGAGCAGCAGCAGCAG 720  
QY 726 CGGGCGATGTCGGCGGAGCAGCGCCAGCGTCCGAGCAGCAGCAGCAGCAGCAGCAG 785  
DB 721 CGGGCGATGTCGGCGGAGCAGCGCCAGCGTCCGAGCAGCAGCAGCAGCAGCAGCAG 780  
QY 786 GACCGCTCGAGTCCAGCCCGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 845  
DB 781 GACCGCTCGAGTCCAGCCCGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 840  
QY 846 GATGGATCTGATCGGCGAGCAGCAGCAAGTAAAGCGTTCGGTTCGATTCGATTCG 905  
DB 841 GATGGATCTGATCGGCGAGCAGCAGCAAGTAAAGCGTTCGGTTCGATTCGATTCG 900  
QY 906 CTGTACAGAGGCATCCGATCCGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 965  
DB 901 CTGTACAGAGGCATCCGATCCGACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 960  
QY 966 ACCCTGGCGTCCAGCGCGTCTGGTCCGCAACCCCGCGCGATGTCGCGCGCGCT 1025  
DB 961 ACCCTGGCGTCCAGCGCGTCTGGTCCGCAACCCCGCGCGATGTCGCGCGCGCT 1020  
QY 1026 CGGCGCGGCTCTCATGGCGGGTTCGTTTCAGTCCGTCGTCGTCGTCGTCGTCGTCG 1085  
DB 1021 CGGCGCGGCTCTCATGGCGGGTTCGTTTCAGTCCGTCGTCGTCGTCGTCGTCGTCG 1080  
QY 1086 GGGCGCGCGCGCTCGTCCGTCGATACGGGATCTATCAGCAGGTCGAGCGGTCGAGCC 1145  
DB 1081 GGGCGCGCGCGCTCGTCCGTCGATACGGGATCTATCAGCAGGTCGAGCGGTCGAGCC 1140  
QY 1146 GTACTCTTTCGCGCCAGAACGCGGTGCGTCGCGCGCAGACAGCGGTCTCTGCGCGCAG 1205  
DB 1141 GTACTCTTTCGCGCCAGAACGCGGTGCGTCGCGCGCAGACAGCGGTCTCTGCGCGCAG 1200  
QY 1206 ATACACCGAGCGGTGGCGGCGATGTCAGATCGTGGCGAGCGCGCGCGCGCGAG 1265  
DB 1201 ATACACCGAGCGGTGGCGGCGATGTCAGATCGTGGCGAGCGCGCGCGCGCGAG 1260

QY 1266 ATCGGATCTATCGCGGCTCTGGCGGAAGCAGAGCGGTAGCGGCTTGCACTACGTC 1325  
DB 1261 ATCGGATCTATCGCGGCTCTGGCGGAAGCAGAGCGGTAGCGGCTTGCACTACGTC 1320  
QY 1326 GCGCGGTTGGCGAGAACGAGACTATCATCGACCGAGCTTTCGCGCAACATCGGGCGTAT 1385  
DB 1321 GCGCGGTTGGCGAGAACGAGACTATCATCGACCGAGCTTTCGCGCAACATCGGGCGTAT 1380  
QY 1386 CTGCCAGTCTGAGTTCGCGCTCTGTCGGATCTATCGCGCACCGCGCCGTCGCGCGC 1445  
DB 1381 CTGCCAGTCTGAGTTCGCGCTCTGTCGGATCTATCGCGCACCGCGCCGTCGCGCGC 1440  
QY 1446 ACCCGGTGGATCGTTCGTCAGTACCCGAGGCTCTTGAGAGCTTAAGCCCAATTGGGAAGAT 1505  
DB 1441 ACCCGGTGGATCGTTCGTCAGTACCCGAGGCTCTTGAGAGCTTAAGCCCAATTGGGAAGAT 1500  
QY 1506 ACTTCGACCTTCCCATCAATAGAGAAAGATCCCTTAGGGATTCGTAGCGGGCCG 1565  
DB 1501 ACTTCGACCTTCCCATCAATAGAGAAAGATCCCTTAGGGATTCGTAGCGGGCCG 1560  
QY 1566 GTGTTTCAGTCAACTTGGCGAGGCAATCCCATCGCGCAGCGCCGCGCAGCGAAATC 1625  
DB 1561 GTGTTTCAGTCAACTTGGCGAGGCAATCCCATCGCGCAGCGCCGCGCAGCGAAATC 1620  
QY 1626 CAC 1628  
DB 1621 CAC 1623

RESULT 6  
US-10-100-679-88  
; Sequence 88, Application US/10100679  
; Publication No. US20030054013A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; TITLE OF INVENTION: and Methods for Their Use  
; FILE REFERENCE: 11000.1042c2  
; CURRENT APPLICATION NUMBER: US/10/100,679  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/351,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 88  
; LENGTH: 1413  
; TYPE: DNA  
; ORGANISM: Mycobacterium vaccae

Query Match 85.4%; Score 1413; DB 14; Length 1413;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATCTACTCGACCTTCGCGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 65  
DB 1 ATCTACTCGACCTTCGCGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 60  
QY 66 CTGGCGACCGCTTCGCGGTTCGCGACGATCAACGCGATGGAAGCAAGGATGTTGGCC 125  
DB 61 CTGGCGACCGCTTCGCGGTTCGCGACGATCAACGCGATGGAAGCAAGGATGTTGGCC 120  
QY 126 AACGCTGCCCGCATCGCGCAGAGGTCTCGACCGGGTCTGCGCGATCTCGCGCCCG 185  
DB 121 AACGCTGCCCGCATCGCGCAGAGGTCTCGACCGGGTCTGCGCGATCTCGCGCCCG 180  
QY 186 CACCGTTCGGTCCGCGAAGTCCGCGCTCTCGCGTCTTCTTGGCGGGATCTGATCCAGAA 245  
DB 181 CACCGTTCGGTCCGCGAAGTCCGCGCTCTTCTTGGCGGGATCTGATCCAGAA 240

QY 246 CGGCGCGTCTGCGGGTTGAGGTCCTCGGTGCCAGTCCGTCGACGCGACGTCGTCCGGC 305  
 Db |||||  
 QY 241 CGGCGCGGTCGCGGGTTGAGGTCCTCGGTGCCAGTCCGTCGACGCGACGTCGTCCGGC 300  
 Db |||||  
 QY 306 GCTGGTGATCGCGCGCGGTAGGCGTCTCGGTCCAAACGTCAGCAACGTCGCGCGGGCG 365  
 Db |||||  
 QY 301 GCTGGTGATCGCGCGCGGTAGGCGTCTCGGTCCAAACGTCAGCAACGTCGCGCGGGCG 360  
 Db |||||  
 QY 366 GATGGATCTATCAGTTCCGCCCTCGGTCCGACGCGCGCGGAGGCGAGCAGTTCCGCTCCG 425  
 Db |||||  
 QY 361 GATGGATCTATCAGTTCCGCCCTCGGTCCGACGCGCGCGGAGGCGAGCAGTTCCGCTCCG 420  
 Db |||||  
 QY 426 GCGTCGATCGGTTGGTTCGTCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 485  
 Db |||||  
 QY 421 GCGTCGATCGGTTGGTTCGTCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 480  
 Db |||||  
 QY 486 GGGTCCCGGACGGTGCAATCTCCAGTCGATGAACCGCGAGCTCGGGAGCGTCGCGCG 545  
 Db |||||  
 QY 481 GGGTCCCGGACGGTGCAATCTCCAGTCGATGAACCGCGAGCTCGGGAGCGTCGCGCG 540  
 Db |||||  
 QY 546 CGCAGCAGCAGTTGTTTCAGATGGCAGTCGCGGTGCAATGATCCCGGGTTCCGGGTTCGTG 605  
 Db |||||  
 QY 541 CGCAGCAGCAGTTGTTTCAGATGGCAGTCGCGGTGCAATGATCCCGGGTTCCGGGTTCGTG 600  
 Db |||||  
 QY 606 GGCCTCGCGAGTCCAGCGAGTCGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 665  
 Db |||||  
 QY 601 GGCCTCGCGAGTCCAGCGAGTCGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 660  
 Db |||||  
 QY 666 GGATCTCATGCTCGGGGAGCGCGGTGCCAGCAACGCCAGCGTGGGAGCAGCAGCAGCAG 725  
 Db |||||  
 QY 661 GGATCTCATGCTCGGGGAGCGCGGTGCCAGCAACGCCAGCGTGGGAGCAGCAGCAGCAG 720  
 Db |||||  
 QY 726 CGGCGCGATGTCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 785  
 Db |||||  
 QY 721 CGGCGCGATGTCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 780  
 Db |||||  
 QY 786 GACCGCTCGGAGTCGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 845  
 Db |||||  
 QY 781 GACCGCTCGGAGTCGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840  
 Db |||||  
 QY 846 GATGGATCTGATCGGCGAGGATCAGCAACAGTAGCGGTGTTCCGGTTGATCCAAATGTG 905  
 Db |||||  
 QY 841 GATGGATCTGATCGGCGAGGATCAGCAACAGTAGCGGTGTTCCGGTTGATCCAAATGTG 900  
 Db |||||  
 QY 906 CTGTCAGCAGCAGTCGATGCGGACCAACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 965  
 Db |||||  
 QY 901 CTGTCAGCAGCAGTCGATGCGGACCAACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 960  
 Db |||||  
 QY 966 ACCCTGGGTCAGCGGGGTCGTGGTCCGCAACCGCGCGCGGATGTCGCGCGCGCGCT 1025  
 Db |||||  
 QY 961 ACCCTGGGTCAGCGGGGTCGTGGTCCGCAACCGCGCGCGGATGTCGCGCGCGCGCT 1020  
 Db |||||  
 QY 1026 CGGCGCGGCTCTCCATGCGCGGTTGTTTTCAGTCGCTGTCGCGGTGGCTGTTCTCGCAACG 1085  
 Db |||||  
 QY 1021 CGGCGCGGCTCTCCATGCGCGGTTGTTTTCAGTCGCTGTCGCGGTGGCTGTTCTCGCAACG 1080  
 Db |||||  
 QY 1086 GGCCTCGCGCGCGCTGTCGTCGCGGATACGGGATCTATCAGCAGGATAGGCGGTCAGGCC 1145  
 Db |||||  
 QY 1081 GGCCTCGCGCGCGCTGTCGTCGCGGATACGGGATCTATCAGCAGGATAGGCGGTCAGGCC 1140  
 Db |||||  
 QY 1146 GTAATCTTTCGCGCGCGGATGTCGTCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1205  
 Db |||||  
 QY 1141 GTAATCTTTCGCGCGCGGATGTCGTCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1200  
 Db |||||  
 QY 1206 ATACACCCAGCGGTGGCGCGCATGTCAGATCTGTCGCGCAGCAGCAGCAGCAGCAGCAGCAG 1265  
 Db |||||  
 QY 1201 ATACACCCAGCGGTGGCGCGCATGTCAGATCTGTCGCGCAGCAGCAGCAGCAGCAGCAGCAG 1260  
 Db |||||  
 QY 1266 ATCGGATCTATCGCGCGGCTGTGCGGAGGAGCAGGCGGTAGCGGGGTTGCACTACGTC 1325  
 Db |||||  
 QY 1261 ATCGGATCTATCGCGCGGCTGTGCGGAGGAGCAGGCGGTAGCGGGGTTGCACTACGTC 1320  
 Db |||||

QY 1326 GCCCGGTTGGCAGAGCAGGACTATCATCGACCGAGCCTTGGCGCAACATCGGGCCGTAT 1385  
 Db |||||  
 QY 1321 GCCCGGTTGGCAGAGCAGGACTATCATCGACCGAGCCTTGGCGCAACATCGGGCCGTAT 1380  
 Db |||||  
 QY 1386 CTGCCAGCTGAGTTCCCGCTCTCGTCGGATCT 1418  
 Db |||||  
 QY 1381 CTGCCAGCTGAGTTCCCGCTCTCGTCGGATCT 1413  
 Db |||||  
 RESULT 7  
 US-10-607-752-88  
 ; Sequence 88, Application US/10607752  
 ; Publication No. US20040072224A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Delcayre, Alain  
 ; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder  
 ; FILE REFERENCE: 11000.1042C3  
 ; CURRENT APPLICATION NUMBER: US/10/607,752  
 ; PRIOR FILING DATE: 2003-06-26  
 ; PRIOR APPLICATION NUMBER: 10/100,679  
 ; PRIOR FILING DATE: 2002-03-14  
 ; PRIOR APPLICATION NUMBER: 09/450,072  
 ; PRIOR FILING DATE: 1999-11-29  
 ; PRIOR APPLICATION NUMBER: 09/351,348  
 ; PRIOR FILING DATE: 1999-07-12  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 88  
 ; LENGTH: 1413  
 ; TYPE: DNA  
 ; ORGANISM: Mycobacterium vaccae  
 US-10-607-752-88  
 Query Match 85.4%; Score 1413; DB 18; Length 1413;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 ATCTACTCGACCTTCGCGGACCGGGGTACCCCGGTGGCTGACGTACTCGGCGCATCCG 65  
 Db |||||  
 QY 1 ATCTACTCGACCTTCGCGGACCGGGGTACCCCGGTGGCTGACGTACTCGGCGCATCCG 60  
 Db |||||  
 QY 66 CTGCGCAGCGCTTCGCGGTTCGCGAGCATCAACGCGATGGAAGCAGGATGTTGGCC 125  
 Db |||||  
 QY 61 CTGCGCAGCGCTTCGCGGTTCGCGAGCATCAACGCGATGGAAGCAGGATGTTGGCC 120  
 Db |||||  
 QY 126 AAGCTGCGCGCATCGCGGAGCAGGTCTCGGACCGGGTCTGCGGATCTCGCGCGCGCG 185  
 Db |||||  
 QY 121 AAGCTGCGCGCATCGCGGAGCAGGTCTCGGACCGGGTCTCGGCGGATCTCGCGCGCGCG 180  
 Db |||||  
 QY 186 CACGTTTCGCTCGCGGAGTCCCGGCTTCGCGGTCTTCTGGCGGGATCTGATCCAGAA 245  
 Db |||||  
 QY 181 CACGTTTCGCTCGCGGAGTCCCGGCTTCGCGGTCTTCTGGCGGGATCTGATCCAGAA 240  
 Db |||||  
 QY 246 CGGCGCGCTCTGCGGGTTGAGGTCTCTCGTTCGCCAGTCCGCTCGACGCGAGTCTCGCG 305  
 Db |||||  
 QY 241 CGGCGCGCTCTGCGGGTTGAGGTCTCTCGTTCGCCAGTCCGCTCGACGCGAGTCTCGCG 300  
 Db |||||  
 QY 306 GCTGGTGATCGCGCGCGGTAGGCGTCTCGGTCCCAACGTCAGCAGCAGTCCCGCGCGCG 365  
 Db |||||  
 QY 301 GCTGGTGATCGCGCGCGGTAGGCGTCTCGGTCCCAACGTCAGCAGCAGTCCCGCGCGCGCG 360  
 Db |||||  
 QY 366 GATGGATCTATCAGTTCCGCCCTCGGTCCGACGCGCGCGGAGGCGAGCAGTTCCGCTCCG 425  
 Db |||||  
 QY 361 GATGGATCTATCAGTTCCGCCCTCGGTCCGACGCGCGCGGAGGCGAGCAGTTCCGCTCCG 420  
 Db |||||  
 QY 426 GCGTCGATCGGTTGGTTCGCTCCGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 485  
 Db |||||  
 QY 421 GCGTCGATCGGTTGGTTCGCTCCGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 480  
 Db |||||  
 QY 486 GGGTCCCGGACGGTGCAATCTCCAGTCGATGAACCGCGAGCTCGGGAGCGTCGCGCG 545  
 Db |||||  
 QY 481 GGGTCCCGGACGGTGCAATCTCCAGTCGATGAACCGCGAGCTCGGGAGCGTCGCGCG 540  
 Db |||||

```

QY 546 CGCAGCAGCAGCTGTTTCAGATGGCAGTCCCGTGCATGATCCCGGTTCCGGTCTGCG 605
Db 541 CGCAGCAGCAGCTGTTTCAGATGGCAGTCCCGTGCATGATCCCGGTTCCGGTCTGCG 600
QY 606 GGCCTCGCAGTCCAGCAGTCCGCGAGCACATGACCGAGCGGGAACGACTCGGCGCG 665
Db 601 GGCCTCGCAGTCCAGCAGTCCGCGAGCACATGACCGAGCGGGAACGACTCGGCGCG 660
QY 666 GGATCTGATCAGTCCGGGAGCGCGGTGCCAGCAACGCGAGCGGTGGGAAGCACCGAGAC 725
Db 661 GGATCTGATCAGTCCGGGAGCGCGGTGCCAGCAACGCGAGCGGTGGGAAGCACCGAGAC 720
QY 726 CGCGCGGATGTCGCCCGCAGCAGCGCCAGCGCGTGCACCCCGCGGAGCGGSCCGCG 785
Db 721 CGCGCGGATGTCGCCCGCAGCAGCGCCAGCGCGTGCACCCCGCGGAGCGGSCCGCG 780
Db 786 GACCGGTTCGAGTGCACCCCGCGCCACCGCGCGCGGTGCTCAGCATCAGCCACCG 845
Db 781 GACCGGTTCGAGTGCACCCCGCGCCAGCGCGCGGTGCTCAGCATCAGCCACCG 840
QY 846 GATGGATCTGATCGGCGAGGATCAGCAACAGTAAGCGGTGTTCCGGTTGAATCCAAATGG 905
Db 841 GATGGATCTGATCGGCGAGGATCAGCAACAGTAAGCGGTGTTCCGGTTGAATCCAAATGG 900
QY 906 CTGTACAGGAGCATCGATGCCGAAACCGACACCGAGCAGTCCGAATCTGTCTCGCG 965
Db 901 CTGTACAGGAGCATCGATGCCGAAACCGACACCGAGCAGTCCGAATCTGTCTCGCG 960
QY 966 ACCCTCGGCTCAGCGCGGTCGTGGCTCCGCAACCGCGCGGATGTCGCGCGCGCGT 1025
Db 961 ACCCTCGGCTCAGCGCGGTCGTGGCTCCGCAACCGCGCGGATGTCGCGCGCGCGT 1020
QY 1026 GCGCGCGGCTCTCCATGGCGGTTCTGATCGTCTGCTCGTCCGTTGCGGAAAG 1085
Db 1021 GCGCGCGGCTCTCCATGGCGGTTCTGATCGTCTGCTCGTCCGTTGCGGAAAG 1080
QY 1086 GCGCGCGGCTCTGCTCGGATCGGATCTATCAGCAGGTAGCGGTCGCGC 1145
Db 1081 GCGCGCGGCTCTGCTCGGATCGGATCTATCAGCAGGTAGCGGTCGCGC 1140
QY 1146 GTACTCTTCCGCCAGAACAGCGGTCCGTCGCGCGCAGACCGCGTCTGCCGCCAG 1205
Db 1141 GTACTCTTCCGCCAGAACAGCGGTCCGTCGCGCGCAGACCGCGTCTGCCGCCAG 1200
QY 1206 ATACACCCAGCGGTGGCGGATGTCAGATCGTGGCGCAGCGCGCGCGGAG 1265
Db 1201 ATACACCCAGCGGTGGCGGATGTCAGATCGTGGCGCAGCGCGCGCGGAG 1260
QY 1266 ATCGGATCTATCGCGGCTGTGGGGAAGGAGCGGCGTAGCGGCTTGCACTACGTC 1325
Db 1261 ATCGGATCTATCGCGGCTGTGGGGAAGGAGCGGCGTAGCGGCTTGCACTACGTC 1320
QY 1326 GCGCGGTTGGCGAGAGCAGGACTATACATCGACCGGCTTGGCAACATCGGCGCGTAT 1385
Db 1321 GCGCGGTTGGCGAGAGCAGGACTATACATCGACCGGCTTGGCAACATCGGCGCGTAT 1380
QY 1386 CTGCGAGTGAAGTTCCCGTCTCTGTCGGATCT 1418
Db 1381 CTGCGAGTGAAGTTCCCGTCTCTGTCGGATCT 1413

```

```

RESULT 8
US-10-100-679-87
; Sequence 87, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c2
; CURRENT APPLICATION NUMBER: US/10/100, 679
; CURRENT FILING DATE: 2002-03-14

```

```

; PRIOR APPLICATION NUMBER: PCT/NZ00/00121
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-10-100-679-87

Query Match 75.3%; Score 1247; DB 14; Length 1263;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1263; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 6 ATCTACTCGACCTTCGCGACCGGCGGTACCCGGGTGGCTGACGTAATCTCCGGCCATCG 65
Db 1 ATCTACTCGACCTTCGCGACCGGCGGTACCCGGGTGGCTGACGTAATCTCCGGCCATCG 60
QY 66 CTGGCGACCGCTCGCGCGTTCGCGATCAACGCGATGCAAGACGAAAGCATGTGTGGCC 125
Db 61 CTGGCGACCGCTCGCGCGTTCGCGATCAACGCGATGCAAGACGAAAGCATGTGTGGCC 120
QY 126 AACGCTGCGCGATCGCGAGCAGTGTCTCGACCGGGTCTCGCGATCTCCGCCCGCG 185
Db 121 AACGCTGCGCGATCGCGAGCAGTGTCTCGACCGGGTCTCGCGATCTCCGCCCGCG 180
QY 186 CACCGTTGCGTCCGCGAAGTCCGCGCTTCGCGGTCTTCGCGCGGATCTGATCCAGAA 245
Db 181 CACCGTTGCGTCCGCGAAGTCCGCGCTTCGCGGTCTTCGCGCGGATCTGATCCAGAA 240
QY 246 CGCGGCGGTCTCGCGGTTCGAGTCTCGGTGCCAGTCCGTCGACGCGACGTCGTCGCG 305
Db 241 CGCGGCGGTCTCGCGGTTCGAGTCTCGGTGCCAGTCCGTCGACGCGACGTCGTCGCG 300
QY 306 GCTGTGATCGCGCGCGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 365
Db 301 GCTGTGATCGCGCGCGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 360
QY 366 GATGATCTATCAGTTCGCGCTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCG 425
Db 361 GATGATC-----TTCGCGCTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCG 414
QY 426 GCGTCGATCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 485
Db 415 GCGTCGATCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 474
QY 486 GCGTCGATCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 545
Db 475 GCGTCGATCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 534
QY 546 CGCAGCAGCAGCTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 605
Db 535 CGCAGCAGCAGCTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 594
QY 606 GCGTCGCGGATTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 665
Db 595 GCGTCGCGGATTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 654
QY 666 GGATCTGATCAGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 725
Db 655 GGATCTGATCAGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 714
QY 726 CGCGCGGATGTCGCCCGCAGCAGCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCG 785
Db 715 CGCGCGGATGTCGCCCGCAGCAGCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCG 774
QY 786 GACCGCGTTCGAGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCG 845
Db 775 GACCGCGTTCGAGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCG 834

```

```

QY      846  GATGGATCTGATCGGCGAGCATCACGAAACAGTAAGCGGTGTTCCGGTTGAATCCAATGTG  905
DB      835  GATGGATCTGATCGGCGAGGCAATCACGAAACAGTAAGCGGTGTTCCGGTTGAATCCAATGTG  894
QY      906  CTGTACAGCAGGATCCGATGCGGAAACACCGAACACCGGAGCAGTCCGAATCTGTCTCGCG  965
DB      895  CTGTACAGCAGGATCCGATGCGGAAACACCGAACACCGGAGCAGTCCGAATCTGTCTCGCG  954
QY      966  ACCCTGGCTCAGCGCGGCTGTTGGCTCCGCAACCGCGCGGATGTCGGCGCGCGCT  1025
DB      955  ACCCTGGCTCAGCGCGGCTGTTGGCTCCGCAACCGCGCGGATGTCGGCGCGCGCT  1014
QY      1026  GCGGCGGCTCTCATGCGCGGTTCTGTTAGTCCGCTCGTCCGCTGCTGTTCTGCGAAACG  1085
DB      1015  GCGGCGGCTCTCATGCGCGGTTCTGTTAGTCCGCTCGTCCGCTGCTGTTCTGCGAAACG  1074
QY      1086  GCGGCGGCTCTCATGCGCGGTTCTGTTAGTCCGCTCGTCCGCTGCTGTTCTGCGAAACG  1145
DB      1075  GCGGCGGCTCTCATGCGCGGTTCTGTTAGTCCGCTCGTCCGCTGCTGTTCTGCGAAACG  1134
QY      1146  GCGGCGGCTCTCATGCGCGGTTCTGTTAGTCCGCTCGTCCGCTGCTGTTCTGCGAAACG  1205
DB      1135  GCGGCGGCTCTCATGCGCGGTTCTGTTAGTCCGCTCGTCCGCTGCTGTTCTGCGAAACG  1194
QY      1206  ATACACCGAGGCGGTGCGCGGATGTCAGATCGTGGCCAGCGCGCGGATGTCGGCGGAG  1265
DB      1195  ATACACCGAGGCGGTGCGCGGATGTCAGATCGTGGCCAGCGCGCGGATGTCGGCGGAG  1254
QY      1266  ATCGGATCT 1274
DB      1255  ATCGGATCT 1263

RESULT 9
US-10-607-752-87
; Sequence 87, Application US/10607752
; Publication No. US20040072224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c3
; CURRENT APPLICATION NUMBER: US/10607,752
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-607-752-87

Query Match      75.3%; Score 1247; DB 18; Length 1263;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1263; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY      6  ATCTACTCGACCTTCGCGCGGCGTACCCGCGGTCGCTGAGCTACTCGGCGCATCCG  65
DB      1  ATCTACTCGACCTTCGCGCGGCGTACCCGCGGTCGCTGAGCTACTCGGCGCATCCG  60
QY      66  CTGCGGACCGCTTCGCGGTCGCGACGATCAACGCGATGGAAGACGAGGATGTCGCGC  125
DB      61  CTGCGGACCGCTTCGCGGTCGCGACGATCAACGCGATGGAAGACGAGGATGTCGCGC  120
QY      126  AACGCTGCCGATCGCGGAGCAGTGTCTCGGACCGGGTCTGCGCGATCTCGCGCGCG  185

```

```

DB      121  AAACGCTGCCGCAATCGGCGAGCAGGTGCTCGAACCGGGTCTCGGCGATCTCGCGCGCG  180
QY      186  CACCGTTCGGTTCGGCGAAATCGCGCGCTTCCTCGCGCGGATCTGATCAGAA  245
DB      181  CACCGTTCGGTTCGGCGAAATCGCGCGCTTCCTCGCGCGGATCTGATCAGAA  240
QY      246  CCGGCGGCTTCGGGTTGAGGTCTCGGTGCGCAAGTCCGCTCGAGCGGATCTGTCGCG  305
DB      241  CCGGCGGCTTCGGGTTGAGGTCTCGGTGCGCAAGTCCGCTCGAGCGGATCTGTCGCG  300
QY      306  GCTGTGATGTCGGCGCGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  365
DB      301  GCTGTGATGTCGGCGCGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  360
QY      366  GATGATCTATCAGTTTCGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  425
DB      361  GATGATCTATCAGTTTCGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  414
QY      426  GGTGATGTCGGGTTGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  485
DB      415  GGTGATGTCGGGTTGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  474
QY      486  GGTGATGTCGGGTTGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  545
DB      475  GGTGATGTCGGGTTGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  534
QY      546  CGCAGCAGCAGCTGTTGTTGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  605
DB      535  CGCAGCAGCAGCTGTTGTTGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  594
QY      606  GGTGATGTCGGGTTGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  665
DB      595  GGTGATGTCGGGTTGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  654
QY      666  GGTGATGTCGGGTTGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  725
DB      655  GGTGATGTCGGGTTGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  714
QY      726  CCGCGCGATGTCGCGCGCAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  785
DB      715  CCGCGCGATGTCGCGCGCAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  774
QY      786  GACCGGTCGGAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG  845
DB      775  GACCGGTCGGAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG  834
QY      846  GATGATCTGATCGGCGAGCAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG  905
DB      835  GATGATCTGATCGGCGAGGATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG  894
QY      906  CTGTACAGCAGGATCCGATGCGGAAACACCGAACACCGGAGCAGTCCGAATCTGTCT  965
DB      895  CTGTACAGCAGGATCCGATGCGGAAACACCGAACACCGGAGCAGTCCGAATCTGTCT  954
QY      966  ACCCTGGCTCAGCGCGGCTGTTGGCTTCGCGAAACCGCGCGGATGTCGGCGCGCG  1025
DB      955  ACCCTGGCTCAGCGCGGCTGTTGGCTTCGCGAAACCGCGCGGATGTCGGCGCGCG  1014
QY      1026  CCGGCGGCTCTCATGCGCGGTTCTGTTAGTCCGCTCGTCCGCTGCTGTTCTGCGAAC  1085
DB      1015  CCGGCGGCTCTCATGCGCGGTTCTGTTAGTCCGCTCGTCCGCTGCTGTTCTGCGAAC  1074
QY      1086  GCGCGCGCGCTCTCATGCGCGGTTCTGTTAGTCCGCTCGTCCGCTGCTGTTCTGCGAAC  1145
DB      1075  GCGCGCGCGCTCTCATGCGCGGTTCTGTTAGTCCGCTCGTCCGCTGCTGTTCTGCGAAC  1134
QY      1146  GTACTCTTCTGCGCGCGGTCGCTGCGCGCGGTCGCGCGGTCGCGCGGTCGCGCG  1205
DB      1135  GTACTCTTCTGCGCGCGGTCGCTGCGCGCGGTCGCGCGGTCGCGCGGTCGCGCG  1194
QY      1206  ATACACCGAGGCGGTGCGCGGATGTCAGATCGTGGCCAGCGCGCGGATGTCGGCGGAG  1265
DB      1195  ATACACCGAGGCGGTGCGCGGATGTCAGATCGTGGCCAGCGCGCGGATGTCGGCGGAG  1254

```



Db 61 CTGGGACCGCCTGCGCGTCCGAGCATCAACGCGATGGAAGCAAGCATGTGGCC 120  
Qy 126 AAGCTGCGCGCATCGCGAGAGAGTGTCTGGACCGGCTCTGGCGATCTCGCGCGCCCG 185  
Db 121 AAGCTGCGCGCATCGCGAGAGAGTGTCTGGACCGGCTCTGGCGATCTCGCGCGCCCG 180  
Qy 186 CACCGTTCCGTCGCGGAAGTCCGCGGCTCGCGGTCTTCTGGCGGATCTGATCCAGAA 245  
Db 181 CACCGTTCCGTCGCGGAAGTCCGCGGCTCGCGGTCTTCTGGCGGATCTGATCCAGAA 240  
Qy 246 CGGCGCGGTCGCGGGTTGAGGTCTCTCGGTGCCAGTCCGTCGACGCGACGTGTCGCGC 305  
Db 241 CGGCGCGGTCGCGGGTTGAGGTCTCTCGGTGCCAGTCCGTCGACGCGACGTGTCGCGC 300  
Qy 306 GCTGGTGATCGCGCGCGCGTAGGGGTCTCGGTCCACAAAGTCAAGCACCGTCCCGGGCG 365  
Db 301 GCTGGTGATCGCGCGCGCGTAGGGGTCTCTCGGTCCACAAAGTCAAGCACCGTCCCGGGCG 360  
Qy 366 GATGGATCTATCAGTTCCGCGCTGTCGCGAGCCCGCGAGGGCAGGCAGTTCGCTCCG 425  
Db 361 GATGGATCTATCAGTTCCGCGCTGTCGCGAGCCCGCGAGGGCAGGCAGTTCGCTCCG 420  
Qy 426 GCGTCGATCGGTTGGTTCGTCGCGCAGCACACAGCATCCACCGAGGTCCAGCAAC 485  
Db 421 GCGTCGATCGGTTGGTTCGTCGCGCAGCACACAGCATCCACCGAGGTCCAGCAAC 480  
Qy 486 GGGTCCCGACGCTGCATCTCCAGTCGATGAAACCGCGGAGCTCGGGGACGTCCGCG 545  
Db 481 GGGTCCCGACGCTGCATCTCCAGTCGATGAAACCGCGGAGCTCGGGGACGTCCGCG 540  
Qy 546 GCGAGCAGCAGTGTTCAGATGCGAGTCCGCTGCATGATCCCGGTTCCGGGTCTCGG 605  
Db 541 GCGAGCAGCAGTGTTCAGATGCGAGTCCGCTGCATGATCCCGGTTCCGGGTCTCGG 600  
Qy 606 GGCCTGCGCAGTCCAGCCAGTCCGCGAGCACATGACCGAGCGGAACGATCCGGCGCG 665  
Db 601 GGCCTGCGCAGTCCAGCCAGTCCGCGAGCACATGACCGAGCGGAACGATCCGGCGCG 660  
Qy 666 GGATCTGATCAGTCTCGGGAGCGGGTCCAGCAACGCGCAGCTGGGAGACCGAGAC 725  
Db 661 GGATCTGATCAGTCTCGGGAGCGGGTCCAGCAACGCGCAGCTGGGAGACCGAGAC 720  
Qy 726 CGGCGCATGTCCCGCGCAGCAGCGCCAGCCGTGACCCCGCGGACCGGGCCCGCG 785  
Db 721 CGGCGCATGTCCCGCGCAGCAGCGCCAGCCGTGACCCCGCGGACCGGGCCCGCG 780  
Qy 786 GACCGCTCGAGTCCGACCCCGCGCGCACCGCGCGCGGTGTCAGCATCAGCCACGG 845  
Db 781 GACCGCTCGAGTCCGACCCCGCGCGCACCGCGCGCGGTGTCAGCATCAGCCACGG 840  
Qy 846 GATGGATCTGATCGCGAGCATACGAAAGTAAAGCGGTTCGTTGAAATCCAAATGTG 905  
Db 841 GATGGATCTGATCGCGAGCATACGAAAGTAAAGCGGTTCGTTGAAATCCAAATGTG 900  
Qy 906 CTGTACGAGCATCCGATCCGAAACCGACCGAGCAGTCCGAAATCTGTCTCGCG 965  
Db 901 CTGTACGAGCATCCGATCCGAAACCGACCGAGCAGTCCGAAATCTGTCTCGCG 960  
Qy 966 ACCCTGGGTCACGCGCGCTGTCGCTCCGAAACCGCGCGGATGTCGCGCGCGCGCT 1025  
Db 961 ACCCTGGGTCACGCGCGCTGTCGCTCCGAAACCGCGCGGATGTCGCGCGCGCGCT 1020  
Qy 1026 CGGCGCGCTCTCCATGCGCGGTTCTGTTTCTGTCGCTGCGGTGTTCTCGGAAAG 1085  
Db 1021 CGGCGCGCTCTCCATGCGCGGTTCTGTTTCTGTCGCTGCGGTGTTCTCGGAAAG 1080  
Qy 1086 GCGCGCGCGCTCTCCATGCGCGGTTCTGTTTCTGTCGCTGCGGTGTTCTCGGAAAG 1121  
Db 1081 GCGCGCGCGCTCTCCATGCGCGGTTCTGTTTCTGTCGCTGCGGTGTTCTCGGAAAG 1116

RESULT 12

US-10-100-679-56  
; Sequence 56, Application US/10100679  
; Publication No. US20030054013A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder  
; FILE REFERENCE: 11000.1042G2  
; CURRENT APPLICATION NUMBER: US/10/100,679  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/351,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 56  
; LENGTH: 1749  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-10-100-679-56  
  
Query Match 61.1%; Score 1011.4; DB 14; Length 1749;  
Best Local Similarity 78.9%; Pred. No. 1.6e-260;  
Matches 1329; Conservative 0; Mismatches 296; Indels 60; Gaps 8;  
  
Qy 1 GATCTATCTACTCGACCTTCGCGACCGGGCGGTACCCGGGTGGCCTGACGTACTCCGGCC 60  
Db 95 GATCTATCTACTCGACCTTCGCGACCGGGCGGTACCCGGGTGGCCTGACGTACTCCGGCC 154  
Qy 61 ATCCGCTGGCGACCGCTTCGCGCGTCCGAGCATCAACGCGATGGAAGAGGCAATGG 120  
Db 155 ATCCGCTGGCGACCGCTTCGCGCGTCCGAGCATCAACGCGATGGAAGAGGCAATGG 214  
Qy 121 TGGCAACGCTGCCCGCATCGCGAGCAGGTGCTCGGACCGGGTCTCGCGATCTCGCCG 180  
Db 215 TGGCAACGCTGCCCGCATCGCGAGCAGGTGCTCGGACCGGGTCTCGCGATCTCGCCG 274  
Qy 181 CCGCGCACCGTTCGCTCGCGCAAGTCCGCGCCTTCGCGGTCTTCCTGGCGGGATCTGATC 240  
Db 275 CCGCGCACCGTTCGCTCGCGCAAGTCCGCGCCTTCGCGGTCTTCCTGGCGGGATCTGATC 334  
Qy 241 CAGAACGGGCGGCTTCGCGGTTGAGGTCTCTCGGTGCCAGTGCCTCGAGCGGACGTCG 300  
Db 335 CAGAACGGGCGGCTTCGCGGTTGAGGTCTCTCGGTGCCAGTGCCTCGAGCGGACGTCG 394  
Qy 301 TCGGCGCTGTGATGCGCGCGCTAGGCGTCTTCGCTCCACACGTCAGCACCGTGGCC 360  
Db 395 TCGGCGCTGTGATGCGCGCGCTAGGCGTCTTCGCTCCACACGTCAGCACCGTGGCC 454  
Qy 361 GGGCGGATGGATCTATCAGTTTCGCGCCTTCGTCGACCGCCCGAGGGCAGCCAGTTCCG 420  
Db 455 GGGCGGATGGATCT----GATCGGAGGATCAGCAACAGTAAGCGGTGTTCCGTTGAA 510  
Qy 421 CTCGGGCGTCGATCGGGTTGGGTCCGTCGGGCGAGCACACGAGATCCACCGAGGTGGA 480  
Db 511 TCCAAATGTGTGTGAGCAGGATCCGA-----TGCAGAACACCGACACCGAGCAGTC 564  
Qy 481 GCAAGGGTCCCGAGCGGTGCATCTCCAGTCGATGAACGCGCGCGAGTCCGGGAGCT 540  
Db 565 GCAATCTGTCTCGGACCCCTGGCGTTCAGCGGCGTCTGTTCCGCAACCCCGCGCGCAT 624  
Qy 541 CGCGCGCAGCAGCAGCTTGTTCAGATGGAGTCCGCGTGCATGATCCCGGTTTCGGCGT 600  
Db 625 GTCGCGCGCGCGT-----GCGCGCGGTCTCTCATGGCGGTTTCGTTTCACT 671  
Qy 601 CGTCGGGCTTCGCGAGTTCAGCGGAGCAGATGTCGGGAGACGATGACCGAGGAGACGATCGG 660  
Db 672 CGCTCGTCCGTTGCTGTTCTGCGAAAGGGGCGCGCGCGCGCTGCTCCG-----TCCG 724

661 GCACGGGATCTGATCACTCGGAGAGCGGGTCCCGAGCAACGCCAGCGTGGGAACACC 720  
Db |||||  
725 ATACGGGATCTGATCACTCGGAGAGCGGGTCCCGAGCAACGCCAGCGTGGGAACACC 784  
Qy |||||  
721 GAGACGGGCGGATGTCGCGGAGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGG 780  
Db |||||  
785 GAGACGGGCGGATGTCGCGGAGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGG 844  
Qy |||||  
781 CCACGGACCGGTCGAGGATCGACCCCGGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGG 840  
Db |||||  
845 CCACGGACCGGTCGAGGATCGACCCCGGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGG 904  
Qy |||||  
841 CACGGATGATCT 896  
Db |||||  
905 CACGGATGATCTATCATGTTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 964  
Qy |||||  
897 TCCAAATGTCTGTCAGCAGCATCCGA-----TGCAGAACCCGACCGAGCAGTC 950  
Db |||||  
965 CTCGGGTCGATCGGTTGGTTCGTCGGCCAGCACACCGATCCACCCGAGTCA 1024  
Qy |||||  
951 GCAATCTCTCGGACCTTGGGTCACGCGGCGTCTGGCTCCGCAACCCCGCGCAT 1010  
Db |||||  
1025 GCAACGGGTCGCCGAGCGTGCACTCTCCAGTCGATGAACCGCGAGCTCGGAGCT 1084  
Qy |||||  
1011 GTCCGGCGCCGCT-----GGGCGGCTCTCCATGGCGGTTGGTTCAGT 1057  
Db |||||  
1085 CGCGGCGCAGCAGCATGTTGTCAGATGGCAGTCGCGCGTCATGATCCCGGGTTCGGCGT 1144  
Qy |||||  
1058 CGTCTGTCGGTGGCTGTTCTGCGAAGCGGCGCGCGCGCGCTCGCG-----TCCG 1110  
Db |||||  
1145 CGTGGGCTGCGGAGTCAGCGAGTCAGCGAGTCGCGGAGCATGACCGAGGAGCATCGG 1204  
Qy |||||  
1111 ATACGGGATCTATCAGCAGGTAGGCGGTCACGCGGTACTCTTCGCCCGCAGAACCGGT 1170  
Db |||||  
1205 GCACGGGATCTATCAGCAGGTAGGCGGTCACGCGGTACTCTTCGCCCGCAGAACCGGT 1264  
Qy |||||  
1171 GCGGTGCGCGCAGACAGCGGTCTCTGCGCAGATACACCGAGGCTGGCGCGCATG 1230  
Db |||||  
1265 GCGGTGCGCGCAGACAGCGGTCTCTGCGCAGATACACCGAGGCTGGCGCGCATG 1324  
Qy |||||  
1231 TCAGATCTGTCGCGCAGCGCGGACAGGTGAGATCGGATCTATCGCGCGCTGTGCG 1290  
Db |||||  
1325 TCAGATCTGTCGCGCAGCGCGGACAGGTGAGATCGGATCTATCGCGCGCTGTGCG 1384  
Qy |||||  
1291 GGAAGGACAGGCGGTAGCGCGCTTGCACTACGTCGCGCGGTTGGCGAAGCAGGACT 1350  
Db |||||  
1385 GGAAGGACAGGCGGTAGCGCGCTTGCACTACGTCGCGCGGTTGGCGAAGCAGGACT 1444  
Qy |||||  
1351 ACATCGACCGGCTTGGCGCAACATCGGCGGCTATCTGCCAGCTGAGGTTCCCGCTCTG 1410  
Db |||||  
1445 ACATCGACCGGCTTGGCGCAACATCGGCGGCTATCTGCCAGCTGAGGTTCCCGCTCTG 1504  
Qy |||||  
1411 TCAGATCTATCGCGCAGCGCGGCGGTCGCGCAGCGGTGATCGTTCGTCACTACC 1470  
Db |||||  
1505 TCAGATCTATCGCGCAGCGCGGCGGTCGCGCAGCGGTGATCGTTCGTCACTACC 1564  
Qy |||||  
1471 CGAAGCTCTTGAAGCTAAGGCCAAATTGGGAAGATCTTGGACTTCCTCCCATCAATAGAGG 1530  
Db |||||  
1565 CGAAGCTCTTGAAGCTAAGGCCAAATTGGGAAGATCTTGGACTTCCTCCCATCAATAGAGG 1624  
Qy |||||  
1531 AAAAGCATCGCCTTAGGGATCTGATAGCGGCGGCGGTTTCGAGTGAATTCGGCAGGG 1590  
Db |||||  
1625 AAAAGCATCGCCTTAGGGATCTGATAGCGGCGGCGGTTTCGAGTGAATTCGGCAGGG 1684  
Qy |||||  
1591 CAATCCCATCGCGGAGCGCGGAGGAAATCCACGGATCCCATCAATCAATCAATC 1650  
Db |||||  
1685 CAATCCCATCGCGGAGCGCGGAGGAAATCCACGGATCCCATCAATCAATCAATC 1744  
Qy |||||  
1651 ACTGA 1655  
Db |||||  
1745 ACTGA 1749

RESULT 13  
US-10-607-752-56  
; Sequence 56, Application US/10607752  
; Publication No. US2004007224A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder;  
; FILE REFERENCE: 11000.1042c3  
; CURRENT APPLICATION NUMBER: US/10/607,752  
; CURRENT FILING DATE: 2003-06-26  
; PRIOR APPLICATION NUMBER: 10/100,679  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/351,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 56  
; LENGTH: 1749  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-10-607-752-56  
  
Query Match 61.1%; Score 1011.4; DB 18; Length 1749;  
Best Local Similarity 78.9%; Pred. No. 1.6e-260;  
Matches 1329; Conservative 0; Mismatches 296; Indels 60; Gaps 8;  
  
Qy 1 GATCTATCTACTCGACCTTCGCGGACCGGCGGTACCGGGTGGCTGAGCTACTCCGGCC 60  
Db 95 GATCTATCTACTCGACCTTCGCGGACCGGCGGTACCGGGTGGCTGAGCTACTCCGGCC 154  
Qy 61 ATCCGCTGCGACCGGCTGCGCGTCCGACCATCAACCGCATGGAAGACGAAGGATGG 120  
Db 155 ATCCGCTGCGACCGGCTGCGCGTCCGACCATCAACCGCATGGAAGACGAAGGATGG 214  
Qy 121 TGGCCAAACGCTCCGCGATCGGACGAGGTGCTCGAACCGGCTTGCAGCATCTCGCG 180  
Db 215 TGGCCAAACGCTCCGCGATCGGACGAGGTGCTCGAACCGGCTTGCAGCATCTCGCG 274  
Qy 181 CCGGCGACCGTTCGCTGCGGAGTCCGCGGCTCGGCGCTCTCTCGGGGGGATCTGATC 240  
Db 275 CCGGCGACCGTTCGCTGCGGAGTCCGCGGCTCGGCGCTCTCTCGGGGGGATCTGATC 334  
Qy 241 CAGAACGGCGCGCTCTCGGGTTGAGGTCTCTCGGTGCCCGAGTGCCTCGACGCGAGTCG 300  
Db 335 CAGAACGGCGCGCTCTCGGGTTGAGGTCTCTCGGTGCCCGAGTGCCTCGACGCGAGTCG 394  
Qy 301 TCGCGCTCGGTGATCGGCGCGCGGTAGGCGTCTCGGTCCAAACCGTCAAGACCGGTGCC 360  
Db 395 TCGCGCTCGGTGATCGGCGCGCGGTAGGCGTCTCGGTCCAAACCGTCAAGACCGGTGCC 454  
Qy 361 GGGCGGATGATCTATCAGTTCGGCCCTGTCGCCAGCCCGCGGAGGCGAGCTTCG 420  
Db 455 GGGCGGATGATCT 510  
Qy 421 CTCGGCGCTCGATCGGGTTGGGTCCGTCGGCGCAGCACACCGAGCATCCACCGAGTCA 480  
Db 511 TCCAAATGCTGTACAGGATCCGA-----TGCAGAACCCGACCCAGCGAGTC 564  
Qy 481 GCAACGGGTCCCGACCGGTGCATCTCCAGTTCGATGAACCGCGGAGCTCGGGGACGT 540  
Db 565 GCAATCTGTCTCGGACCCCTGGCGTCAAGCGGCTGCTGGCTCCGCAACCGCGCGGAT 624  
Qy 541 CCGGGCGGACGACGATGTTTTCAGATGGCAGTTCGCGCTGATGATCCCGGGTTCGCGCT 600  
Db 625 GTCCGCGCGCGCT-----GGGCGGCGCTCTCCATGGCGGCTTCGTTGAT 671  
Qy 601 CGTCCGGCTTCGCGAGTCCAGCTCGGCGGAGCATGTCACCGAGCGGAGCTCGG 660



Db 601 GGCTTGGCGAGTCCAGCCAGTCCGGCGAGCACAATGACCGAGCGGAACGACTCGGGCGG 660  
QY 666 GGATCTGATCAGCTCGGGAGCCGGGTGCCAGCAACCGCAGCGTGGGAAGCACCAGAC 725  
Db 661 GGATCTGATCAGCTCGGGAGCCGGGTGCCAGCAACCGCAGCGTGGGAAGCACCAGAC 720  
QY 726 CGGCGGATGTGCCCGGAGCAGCCCGCAGCCGCTGCACCCCGGGAGCCGGGCCCGG 785  
Db 721 CGGCGGATGTGCCCGGAGCAGCCCGCAGCCGCTGCACCCCGGGAGCCGGGCCCGG 780  
QY 786 GACCGGTTCGAGTCCAGCCCGCCAGCCCGCGCGTGGTTCAGCATCAGCCACCG 845  
Db 781 GACCGGTTCGAGTCCAGCCCGCCAGCCCGCGCGTGGTTCAGCATCAGCCACCG 840  
QY 846 GAT 848  
841 GAT 843

RESULT 15  
US-10-607-752-85  
; Sequence 85, Application US/10607752  
; Publication No. US20040072224A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; FILE REFERENCE: 11000.1042c3  
; CURRENT APPLICATION NUMBER: US/10/607,752  
; CURRENT FILING DATE: 2003-06-26  
; PRIOR APPLICATION NUMBER: 10/100,679  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/351,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 85  
; TYPE: DNA  
; ORGANISM: Mycobacterium vaccae  
US-10-607-752-85

Query Match 50.9%; Score 843; DB 18; Length 843;  
Best Local Similarity 100.0%; Pred. No. 1.7e-215;  
Matches 843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 6 ATCTACTCGACCTTCGCCGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 65  
Db 1 ATCTACTCGACCTTCGCCGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 60  
QY 66 CTGGCGACCGCCTGCGCGTTCGGACGATCAACCGCGATGGAAGACGAAGGCATGTGGCC 125  
Db 61 CTGGCGACCGCCTGCGCGTTCGGACGATCAACCGCGATGGAAGACGAAGGCATGTGGCC 120  
QY 126 AAGCTTCCCGCATCGCGAGCAGTCTCGGACCGGGTCTGCGGATCTCGCGGCCCGG 185  
Db 121 AAGCTTCCCGCATCGCGAGCAGTCTCGGACCGGGTCTGCGGATCTCGCGGCCCGG 180  
QY 186 CACGGTTTCGGTCGGCGAAGTCCCGCGCTCGGGTCTTCTGGCGGGATCTGATCCAGAA 245  
Db 181 CACGGTTTCGGTCGGCGAAGTCCCGCGCTCGGGTCTTCTGGCGGGATCTGATCCAGAA 240  
QY 246 CGGCGCGGTCTGCGGGTTGAGGTCTCTCGGTGCCAGTCCGCTCGACCGCACGTCGTGGC 305  
Db 241 CGGCGCGGTCTGCGGGTTGAGGTCTCTCGGTGCCAGTCCGCTCGACCGCACGTCGTGGC 300  
QY 306 GCTGGTGTATGCGGGCCCGGTAGGGTCTCTCGGTGCCAGTCCGCTCGACCGCACGTCGTGGC 365  
Db 301 GCTGGTGTATGCGGGCCCGGTAGGGTCTCTCGGTGCCAGTCCGCTCGACCGCACGTCGTGGC 360

QY 366 GATGATCTATCAGTTCCGGCCTGTGCGACCGCCGAGGGCAGCCAGTTCCGCTCCG 425  
Db 361 GATGATCTATCAGTTCCGGCCTGTGCGACCGCCGAGGGCAGCCAGTTCCGCTCCG 420  
QY 426 GCGTCGATCGGGTTCGGTCCGGCCAGCAACACAGCATCCACCCGAGGTTCGAGCAAC 485  
Db 421 GCGTCGATCGGGTTCGGTCCGGCCAGCAACACAGCATCCACCCGAGGTTCGAGCAAC 480  
QY 486 GGGTCCCGACCGTTCACATCTCCAGTCCGATGAAACCGCGAGCTCCGGGACGTCGCG 545  
Db 481 GGGTCCCGACCGTTCACATCTCCAGTCCGATGAAACCGCGAGCTCCGGGACGTCGCG 540  
QY 546 CGCAGCAGCACGTTGTTTCAGATGCGCGTGCATGATCCCGGGTTCGGGCTCGTCG 605  
Db 541 CGCAGCAGCACGTTGTTTCAGATGCGCGTGCATGATCCCGGGTTCGGGCTCGTCG 600  
QY 606 GGCCTGCGCAGTCCAGCCAGTCCGGGAGCAATGACCCGAGCGGAAACGACTCCGGCGCG 665  
Db 601 GGCCTGCGCAGTCCAGCCAGTCCGGGAGCAATGACCCGAGCGGAAACGACTCCGGCGCG 660  
QY 666 GGATCTGATCAGTCCGGGAGCCGGGTGCCAGCAACCGCAGCTGGGAAAGCACCAGAC 725  
Db 661 GGATCTGATCAGTCCGGGAGCCGGGTGCCAGCAACCGCAGCTGGGAAAGCACCAGAC 720  
QY 726 CGGCGCATGTGCTCCGCGCAGCAGCGCCCGCAGCCCGTGCACCCCGCGGACCCGGCCCCGCG 785  
Db 721 CGGCGCATGTGCTCCGCGCAGCAGCGCCCGCAGCCCGTGCACCCCGCGGACCCGGCCCCGCG 780  
QY 786 GACCGGTTCGAGTTCGACCCCGCGCGCAACCGCGCGCGTGGTTCAGCATCAGCCACCG 845  
Db 781 GACCGGTTCGAGTTCGACCCCGCGCGCAACCGCGCGCGTGGTTCAGCATCAGCCACCG 840  
QY 846 GAT 848  
841 GAT 843

Search completed: October 7, 2005, 00:25:23  
Job time : 1120 secs

U

QY 361 GGGGGATGGATCTATCAGTTCCGGCCCTGGTCCGACGCCCGGAGGGCAGCCAGTTCCG 420  
 Db 455 GGGCGGATGGATCTATCAGTTCCGGCCCTGGTCCGACGCCCGGAGGGCAGCCAGTTCCG 514  
 QY 421 CTCGGCGTCCGATCGGTTGGGTCCTGCGCGCCAGACACACGATCCACCCGAGGTCCA 480  
 Db 515 CTCGGCGTCCGATCGGTTGGGTCCTGCGCGCCAGACACACGATCCACCCGAGGTCCA 574  
 QY 481 GCAACGGGTCCTCCGACGGTGCACATCTCCAGTTCGATGAACGCGCGAGCTCCGGGACGT 540  
 Db 575 GCAACGGGTCCTCCGACGGTGCACATCTCCAGTTCGATGAACGCGCGAGCTCCGGGACGT 634  
 QY 541 CGCGGCGCAGCAGCAGTGGTTTCAGATGGGAGTCCGCGTGCATGATCCCGGTTCCGGCT 600  
 Db 635 CGCGGCGCAGCAGCAGTGGTTTCAGATGGGAGTCCGCGTGCATGATCCCGGTTCCGGCT 694  
 Db 601 CGTCGGGCTTCGCGAGTCCAGCAGTCGCGGAGCAGCATGCAACCGGGAACGATCCG 660  
 Db 695 CGTCGGGCTTCGCGAGTCCAGCAGTCGCGGAGCAGCATGCAACCGGGAACGATCCG 754  
 QY 661 GCGCGGATCTGATCAGTCCGGGAGCGCGGTGCCAGCAACGCCAGCGTGGGAAGCACC 720  
 Db 755 GCGCGGATCTGATCAGTCCGGGAGCGCGGTGCCAGCAACGCCAGCGTGGGAAGCACC 814  
 QY 721 GAGACGGGCGGATGTCGCGCGCAGCAGCGCCAGCGTGCACCCCGGCGGACCGGGCC 780  
 Db 815 GAGACGGGCGGATGTCGCGCGCAGCAGCGCCAGCGTGCACCCCGGCGGACCGGGCC 874  
 QY 781 CCGCGGACCGGTCGGAGTCCAGCCCGCGCGCCAGCCCGCGCGTGTGTCAGCATCAGC 840  
 Db 875 CCGCGGACCGGTCGGAGTCCAGCCCGCGCGCCAGCCCGCGCGTGTGTCAGCATCAGC 934  
 QY 841 CACGGGATGGATCTGATTCGGCAGGATTCAGAAAGTAAAGCGGTGTTCCGGTTGAATCCA 900  
 Db 935 CACGGGATGGATCTGATTCGGCAGGATTCAGAAAGTAAAGCGGTGTTCCGGTTGAATCCA 994  
 QY 901 ATGTCGTTCAGCAGGATCCGATGCGAACCGGACCGGAGCAGTCCGATCTGTC 960  
 Db 995 ATGTCGTTCAGCAGGATCCGATGCGAACCGGACCGGAGCAGTCCGATCTGTC 1054  
 QY 961 TCGCGACCTTCGGGTCACGCGGCGTTCGTGCTCCGCAACCGCGCGGATGTCGCGCGG 1020  
 Db 1055 TCGCGACCTTCGGGTCACGCGGCGTTCGTGCTCCGCAACCGCGCGGATGTCGCGCGG 1114  
 Db 1021 CCGGTCGGGCGGCTTCATAGCGCGGTTCCGTTAGTCGTCGTCGTCGTCGTCGTCGTCG 1080  
 Db 1115 CCGGTCGGGCGGCTTCATAGCGCGGTTCCGTTAGTCGTCGTCGTCGTCGTCGTCGTCG 1174  
 QY 1081 GAACGGGCGCGCGCGGTCGTCGTCGATACGGGATCTATCAGCAGGTAGGCGGTC 1140  
 Db 1175 GAACGGGCGCGCGCGGTCGTCGTCGATACGGGATCTATCAGCAGGTAGGCGGTC 1234  
 QY 1141 CAGCGGTACTCTTCGCGCCCAAGACAGCGGTCCGTCGCGCGCAGACGCGTCTCTGCC 1200  
 Db 1235 CAGCGGTACTCTTCGCGCCCAAGACAGCGGTCCGTCGCGCGCAGACGCGTCTCTGCC 1294  
 QY 1201 GCAGATACACCGAGCGGTGGCGGATGTCAGATTCGTCGTCGCGCGCAGCGGCGGACGG 1260  
 Db 1295 GCAGATACACCGAGCGGTGGCGGATGTCAGATTCGTCGTCGCGCGCAGCGGCGGACGG 1354  
 QY 1261 TGGAGATTCGATCTATTCGCGCGGTCGTGGGAAGGACGAGGCGGTAGCGCGTTCGACT 1320  
 Db 1355 TGGAGATTCGATCTATTCGCGCGGTCGTGGGAAGGACGAGGCGGTAGCGCGTTCGACT 1414  
 QY 1321 ACGTCCGCGCGGTGGGAGAGCAGGACTATACGACCGAGCTTCGCAACATCGGGC 1380  
 Db 1415 ACGTCCGCGCGGTGGGAGAGCAGGACTATACGACCGAGCTTCGCAACATCGGGC 1474  
 QY 1381 CGTATTCGACGCTGAGGTTCCGCTCTCGTCGATCTATCGCGGCAACCGGCGCGGTGC 1440  
 Db 1475 CGTATTCGACGCTGAGGTTCCGCTCTCGTCGATCTATCGCGGCAACCGGCGCGGTGC 1534

QY 1441 CCGGACCGCGTGGATCGTTCTCAGTACCCGAGAGCTCTTGAGAGCTAAGGCAATTGGG 1500  
 Db 1535 CCGGACCGCGTGGATCGTTCTCAGTACCCGAGAGCTCTTGAGAGCTAAGGCAATTGGG 1594  
 QY 1501 AAGATACTTTGGACCTTTCCCATCAATAGAGAAAAGCATCGCCTAGGGGATCCGTAGCGG 1560  
 Db 1595 AAGATACTTTGGACCTTTCCCATCAATAGAGAAAAGCATCGCCTAGGGGATCCGTAGCGG 1654  
 QY 1561 GCCCGGTTCCTGAGTGAACCTTGGGAGGCAATCCCATCGCGGAGCCGCGAGCGG 1620  
 Db 1655 GCCCGGTTCCTGAGTGAACCTTGGGAGGCAATCCCATCGCGGAGCCGCGAGCGG 1714  
 QY 1621 AAATCCAGCGATCCCATCACCATCACCATCTGTA 1655  
 Db 1715 AAATCCAGCGATCCCATCACCATCACCATCTGTA 1749

RESULT 2  
 US-09-351-348-58  
 ; Sequence 58, Application US/09351348  
 ; Patent No. 6436898  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Delcayre, Alain  
 ; TITLE OF INVENTION: Compounds and Methods for the Treatment  
 ; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines  
 ; FILE REFERENCE: 11000.1042  
 ; CURRENT APPLICATION NUMBER: US/09/351,348  
 ; CURRENT FILING DATE: 1999-07-12  
 ; NUMBER OF SEQ ID NOS: 81  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 58  
 ; LENGTH: 1749  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Made in a lab  
 US-09-351-348-58

Query Match 100.0%; Score 1655; DB 3; Length 1749;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCTATCTACTCGACCTTCGCGGCGACCGGCGGTACCGCGGTGGCTCTGAGCTCTCGGCG 60  
 Db 95 GATCTATCTACTCGACCTTCGCGGCGACCGGCGGTACCGGCGGTGGCTCTGAGCTCTCGGCG 154  
 QY 61 ATCCGCTGCGGACCGGCTTCGCGGCTCGGACGATCAACCGGATGGAAGACGAAGGATGG 120  
 Db 155 ATCCGCTGCGGACCGGCTTCGCGGCTCGGACGATCAACCGGATGGAAGACGAAGGATGG 214  
 QY 121 TGGCCAAACGCTCGCGCATCGCGGAGCGGTCTCGGACCGGCTCTCGCGGATCTCGCGG 180  
 Db 215 TGGCCAAACGCTCGCGCATCGCGGAGCGGTCTCGGACCGGCTCTCGCGGATCTCGCGG 274  
 QY 181 CCGCGCACCGCTTCGCTCGCGGAGTCCGCGGCTCTCGCGCTCTTTGCGGCGGATCTGATC 240  
 Db 275 CCGCGCACCGCTTCGCTCGCGGAGTCCGCGGCTCTCGCGCTCTTTGCGGCGGATCTGATC 334  
 QY 241 CAGAACCGGCGCGGTCTCGCGGTTGAGTCTCTCGGTCCGAGTCCGCTCGACGCGAGCTCG 300  
 Db 335 CAGAACCGGCGCGGTCTCGCGGTTGAGTCTCTCGGTCCGAGTCCGCTCGACGCGAGCTCG 394  
 QY 301 TCGCGGCTGCTGATCGCGGCGCGGTAGGCGTCTCGGTCCACAACTCAGACCGGTGCC 360  
 Db 395 TCGCGGCTGCTGATCGCGGCGCGGTAGGCGTCTCTCGGTCCACAACTCAGACCGGTGCC 454  
 QY 361 GGGCGGATGGATCTATCAGTTCCGGCTTCGTCGACCGCGCGGAGGCGAGCTTCG 420  
 Db 455 GGGCGGATGGATCTATCAGTTCCGGCTTCGTCGACCGCGCGGAGGCGAGCTTCG 514  
 QY 421 CTCGCGGCTGATCGGGTTGGGTCGTCGCGGCGAGCAGACCGAGCATCCACCGGAGTCCA 480  
 Db 515 CTCGCGGCTGATCGGGTTGGGTCGTCGCGGCGAGCAGACCGAGCATCCACCGGAGTCCA 574

Qy 481 GCACCGGTCCCGACGGTGCACATCTCCAGTCGATGAACCGCGGAGCTCGGGACGT 540  
Db 575 GCACCGGTCCCGACGGTGCACATCTCCAGTCGATGAACCGCGGAGCTCGGGACGT 634  
Qy 541 CGCGGCGCAGCAGCAGCTTTGTTTCAGATGGCAGTCGCGGTGCATGATCCCGGGTTTCGGCGT 600  
Db 635 CGCGGCGCAGCAGCAGCTTTGTTTCAGATGGCAGTCGCGGTGCATGATCCCGGGTTTCGGCGT 694  
Qy 601 CFTCGGCGTCCCGAGTCCAGCCAGTCGCGGAGCACTGCACCGGGAACGATCTCG 660  
Db 695 CFTCGGCGTCCCGAGTCCAGCCAGTCGCGGAGCACTGCACCGGGAACGATCTCG 754  
Qy 661 GCGCGGATCTGATCAGCTCGGGAGCGGGTCCCGAGCAACCGCGGAGCTGGGAACACC 720  
Db 755 GCGCGGATCTGATCAGCTCGGGAGCGGGTCCCGAGCAACCGCGGAGCTGGGAACACC 814  
Qy 721 GAGACCGGCGGATGTGCCCGCGCAGCAGCGCCAGCCGTGCAACCCCGGGGACCGGGCC 780  
Db 815 GAGACCGGCGGATGTGCCCGCGCAGCAGCGCCAGCCGTGCAACCCCGGGGACCGGGCC 874  
Qy 781 CC CGGACCGCGTCCGAGTCAACCCCGGCGCCAGCCCGCGCGCGTGTGTCAGCATCAGC 840  
Db 875 CC CGGACCGCGTCCGAGTCAACCCCGGCGCCAGCCCGCGCGCGTGTGTCAGCATCAGC 934  
Qy 841 CACGGATGATCTGATCCGAGGCACTCAGACAGTACGCGGTTCGCGTTGAATCCA 900  
Db 935 CACGGATGATCTGATCCGAGGCACTCAGACAGTACGCGGTTCGCGTTGAATCCA 994  
Qy 901 ATGTGCTGCAGCAGGATCCGATGCCGAACACCGACCGCAGCAGTCGCAATCTGTC 960  
Db 995 ATGTGCTGCAGCAGGATCCGATGCCGAACACCGACCGCAGCAGTCGCAATCTGTC 1054  
Qy 961 TC CGGACCCCTGGCGTCAACCGCGCGTGTGCTCCGAACCCCGCGCGATGTCCGGCGG 1020  
Db 1055 TC CGGACCCCTGGCGTCAACCGCGCGTGTGCTCCGAACCCCGCGCGATGTCCGGCGG 1114  
Qy 1021 CCGGTGGCGCGGTCTCCATGCGCGGTTCGTTTCAGTCGCTCCGTCCGTGGCTGTTGTC 1080  
Db 1115 CCGGTGGCGCGGTCTCCATGCGCGGTTCGTTTCAGTCGCTCCGTCCGTGGCTGTTGTC 1174  
Qy 1081 GACCGGCGCGCGCGCGCTCGTCCGTCCGATACGGGATCTATCAGCAGGTAGCGGTC 1140  
Db 1175 GACCGGCGCGCGCGCGCTCGTCCGTCCGATACGGGATCTATCAGCAGGTAGCGGTC 1234  
Qy 1141 CAGCGGTACTTTTCGCCCGCAGAACAGCGGTGCGCGCGCAGACCGGTCCTGCC 1200  
Db 1235 CAGCGGTACTTTTCGCCCGCAGAACAGCGGTGCGCGCGCAGACCGGTCCTGCC 1294  
Qy 1201 GCCAGATACACCGCGGTGGCGCGCATGTCAGATCGTGGCGCAGCGCGCGGACCG 1260  
Db 1295 GCCAGATACACCGCGGTGGCGCGCATGTCAGATCGTGGCGCAGCGCGCGGACCG 1354  
Qy 1261 TGGAGATCGGATCTATCGCGCGCTGTGCGGAGAGCAGAGCGCTAGCGCGCTTGCACT 1320  
Db 1355 TGGAGATCGGATCTATCGCGCGCTGTGCGGAGAGCAGAGCGCTAGCGCGCTTGCACT 1414  
Qy 1321 AC GTCGCCCGGTTGGCGAGAGCAGGACTACATCGACCGAGCTTCGCGCAACATCGGGC 1380  
Db 1415 AC GTCGCCCGGTTGGCGAGAGCAGGACTACATCGACCGAGCTTCGCGCAACATCGGGC 1474  
Qy 1381 CGTATCTGCAGCTGAGTTCCCGCTCTCGTCGATCTATCGCGCGCAGCGCGCGGTC 1440  
Db 1475 CGTATCTGCAGCTGAGTTCCCGCTCTCGTCGATCTATCGCGCGCAGCGCGCGGTC 1534  
Qy 1441 CCGGACCGCGTGTGATCTTCGTTCAGTACCGGAGCTCTTCAGAGCTTAAGGCCAATTTGGG 1500  
Db 1535 CCGGACCGCGTGTGATCTTCGTTCAGTACCGGAGCTCTTCAGAGCTTAAGGCCAATTTGGG 1594  
Qy 1501 AAGATCTTGGACCTTCCCATCAATAGAGGAAAGCATCGCCCTAGGGGATTCCTAGCGG 1560  
Db 1595 AAGATCTTGGACCTTCCCATCAATAGAGGAAAGCATCGCCCTAGGGGATTCCTAGCGG 1654

Qy 1561 GCCCGGTGTTTCAGTGAACCTTGGCGAGGCAATCCCATCGCGCGAGCCCGCGAGCGG 1620  
Db 1655 GCCCGGTGTTTCAGTGAACCTTGGCGAGGCAATCCCATCGCGCGAGCCCGCGAGCGG 1714  
Qy 1621 AAATCCAGGATCCCATCACCATCACCATCACTGA 1655  
Db 1715 AAATCCAGGATCCCATCACCATCACCATCACTGA 1749  
RESULT 3  
US-09-450-072-56  
; Sequence 56, Application US/09450072  
; Patent No. 6358734  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder:  
; TITLE OF INVENTION: and Methods for Their Use  
; FILE REFERENCE: 11000.1042c1  
; CURRENT APPLICATION NUMBER: US/09/450,072  
; EARLIER FILING DATE: 1999-11-29  
; EARLIER APPLICATION NUMBER: 09/351,348  
; EARLIER FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 56  
; LENGTH: 1749  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-450-072-56  
Query Match 61.1%; Score 1011.4; DB 3; Length 1749;  
Best Local Similarity 78.9%; Pred. No. 3.5e-213;  
Matches 1329; Conservative 0; Mismatches 296; Indels 60; Gaps 8;  
Qy 1 GATCTATCTACTCGACCTTTTCGCGACCGCGGCTACCGGGTGGCCTTGAGCTACTCGGCC 60  
Db 95 GATCTATCTACTCGACCTTTTCGCGACCGCGGCTACCGGGTGGCCTTGAGCTACTCGGCC 154  
Qy 61 ATCCGCTGGCGACCGCGCTCGCGGTCGCGACGATCAACCGATGGAAGAGCAAGGATGG 120  
Db 155 ATCCGCTGGCGACCGCGCTCGCGGTCGCGACGATCAACCGATGGAAGAGCAAGGATGG 214  
Qy 121 TGCGCAACCGCTGCCCGCATCGCGACGAGTGTCTCGGAACCGGGTCTCGCGATCTCGCCG 180  
Db 215 TGCGCAACCGCTGCCCGCATCGCGACGAGTGTCTCGGAACCGGGTCTCGCGATCTCGCCG 274  
Qy 181 CCGGCAACCGTTCGCTCGCGGAAAGTCCCGGCTCGCGGCTCTTCTGGGCGGGATCTGATC 240  
Db 275 CCGGCAACCGTTCGCTCGCGGAAAGTCCCGGCTCGCGGCTCTTCTGGGCGGGATCTGATC 334  
Qy 241 CAGAACCGGCGCGTCTCGCGGTTGAGTCTCGGTGCCAGTCCCGTCCGACGAGCTCG 300  
Db 335 CAGAACCGGCGCGTCTCGCGGTTGAGTCTCGGTGCCAGTCCCGTCCGACGAGCTCG 394  
Qy 301 TC CGCGCTGTGATGCGCGCGCTAGGCGTCTCGGTCCCAACCGTTCAGCAACCGTCCCG 360  
Db 395 TC CGCGCTGTGATGCGCGCGCTAGGCGTCTCGGTCCCAACCGTTCAGCAACCGTCCCG 454  
Qy 361 GCGCGGATGATCTATCAGTTTCGCGCTCGCGCTCGCGGCTCGCGGAGCGGATTCGCG 420  
Db 455 GCGCGGATGATCTATCAGTTTCGCGCTCGCGCTCGCGGCTCGCGGAGCGGATTCGCG 510  
Qy 421 CTC CGGCGTTCGAGTTGGGTTCGCTCGCGGCGAGCACACGATCCACCGGAGTTCGA 480  
Db 511 TC CAATGTGCTGTCAGCAGGATCCGA-----TGCGCAACACGACGACGCGAGTGC 564  
Qy 481 GCAACGGTCCCGACCGGTGCATCTCCAGTGCATGAACCGCGCGAGCTTCGGGGAGCT 540  
Db 565 GCAATGTCTCGCGACCCCTGGGCTACCGCGGCTCGTGGCTCGCGCAACCGCGCGGAT 624  
Qy 541 CGCGGCGCAGCAGCAGCTTGTTCAGATGGCAGTCCCGCTGCGATGATCCCGGGTTTCGGGT 600

```

Db      625  GTCCGCGCGCCGCT-----GGGCGCGGCTCTCCATGCGCGGTTGTTCACT 671
QY      601  CGTCGGGCTGCGCGAGTCCAGCACTGCGCGAGCAATGCAACCGAGGAAAGCACTCGG 660
Db      672  CGCTCGTCCGGTGGCTGTTCTGCGAAGCGGCGCGCGCGCGCTCGTCCG-----TCCG 724
QY      661  GCGCGGGATCTGATCAGCTCGGGAGCGCGGGTCCAGCAACCGCAAGCGTGGGAAGCAC 720
Db      725  ATACGGGATCTGATCAGCTCGGGAGCGCGGGTCCAGCAACCGCAAGCGTGGGAAGCAC 784
QY      721  GAGACCGGCGGATGTCGCGCGCAGCAGCGCGCGCGCGTGCACCCCGCGGAGCGCGGCG 780
Db      785  GAGACCGGCGGATGTCGCGCGCAGCAGCGCGCGCGCGTGCACCCCGCGGAGCGCGGCG 844
QY      781  CCGCGGACCGCGTGGAGTGCACCCCGCGCGCGCACCGCGCGCGCGTGTGTCAAGTACAG 840
Db      845  CCGCGGACCGCGTGGAGTGCACCCCGCGCGCGCACCGCGCGCGCGTGTGTCAAGTACAG 904
QY      841  CAGCGGATGATCT---GATCGCGAGGATCAGCAACAGTAGCGGTGTTCCGTTGAA 896
Db      905  CACGGATGATCTATCAGTTCGGCCCTCGTCCAGCGCGCGCGCGGAGCGAGCGAGTTCG 964
QY      897  TCCAAATGTGTGTCAGCAGGATCCGA-----TGCAGAACCGCACCGCAGCAGTTC 950
Db      965  CTCGGGCTCGATCGGGTGGTCCGTCCGGCGCAGCACACCGATCCACCGGAGTCA 1024
QY      951  GCAATCTGTCTCCGACCCCTGGCGTCAACCGCGCGTGTGGTCCGCAACCGCGCGGAT 1010
Db      1025  GCAACGGTCCCGCAGCGGTGCATCTCCAGTGCATGAACCGCGCGAGTCCGGGACGT 1084
QY      1011  GTCCGCGCGCGCT-----GGGCGCGCTCTCCATGCGCGGTTGTTCACT 1057
Db      1085  CGCGGCGCAGCAGCAGTGTTCAGATGGCAGTCCGCGTGCATGATCCCGGGTTCGGCG 1144
QY      1058  CGCTCGTCCGGTGGCTGTTCTGCGAAGCGGCGCGCGCGCGCGTTCGTCG-----TCCG 1110
Db      1145  CGTCCGGCTCGCGGATCCAGCGTCCAGCGTGGGAGCAGATGCACCGAGGAGCAGTCCG 1204
QY      1111  ATACGGGATCTATCAACGAGTGGCGTCCAGCGTGTCTTTCCGCGCGCAGAACAGCGGT 1170
Db      1205  GCGCGGATCTATCAACGAGTGGCGTCCAGCGTGTCTTTCCGCGCGCAGAACAGCGGT 1264
QY      1171  GCGTCCGCGCGCAGACCGCGTCTGCGCGCAGATACACCGAGCGGTGGCGCGCATG 1230
Db      1265  GCGTCCGCGCGCAGACCGCGTCTGCGCGCAGATACACCGAGCGGTGGCGCGCATG 1324
QY      1231  TCCAGATCTGTGGCGCAGCGCGCGCAGCGTGGAGATCGGATCTATCGCGCGCTGTGCG 1290
Db      1325  TCCAGATCTGTGGCGCAGCGCGCGCAGCGTGGAGATCGGATCTATCGCGCGCTGTGCG 1384
QY      1291  GGAAGCAGAGCGCGTGTGCACTACGTCGCGCGCGTGGAGATCGGATCTATCGCGCGCT 1350
Db      1385  GGAAGCAGAGCGCGTGTGCACTACGTCGCGCGCGTGGAGATCGGATCTATCGCGCGCT 1444
QY      1351  ACATCGACCGAGCTTTCGCAACATCGGCGCGTATCTGCGAGTGGAGTTCGCGCTCG 1410
Db      1445  ACATCGACCGAGCTTTCGCAACATCGGCGCGTATCTGCGAGTGGAGTTCGCGCTCG 1504
QY      1411  TCGGATCTATCGCGCGCAGCGCGCGCGTGGCGCGCGTGGATCGTTCGTCAGTACC 1470
Db      1505  TCGGATCTATCGCGCGCAGCGCGCGCGTGGCGCGCGTGGATCGTTCGTCAGTACC 1564
QY      1471  CGAAGCTCTTGAGAGTAAAGCCAAATGGGAAGATATTTGGAATCTTCCATCAATAGAG 1530
Db      1565  CGAAGCTCTTGAGAGTAAAGCCAAATGGGAAGATATTTGGAATCTTCCATCAATAGAG 1624
QY      1531  AAAAGCATCCCTTAGGGATCGTAGCGCGCGCGTGTTCGAGTGAACCTTCGGCAGAG 1590
Db      1625  AAAAGCATCCCTTAGGGATCGTAGCGCGCGCGTGTTCGAGTGAACCTTCGGCAGAG 1684
QY      1591  CAATCCCATCGCGCAGCGCGCGCGGAGTCCAGGATCCCAATCAACCATCAATCAATC 1650

```

```

Db      1685  CAATCCCATCGCGCAGCGCGCGGAGAAATCCAGGATCCCATCACCATCACCATC 1744
QY      1651  ACTGA 1655
Db      1745  ACTGA 1749

RESULT 4
US-09-351-348-56
; Sequence 56, Application US/09351348
; Patent No. 6436898
; GENERAL INFORMATION:
; APPLICANT: Delcavre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; OF MYCOBACTERIAL INFECTIONS WITH MULTI-EPIOTOPE VACCINES
; FILE REFERENCE: 11000.1042
; CURRENT APPLICATION NUMBER: US/09/351,348
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; TYPE: DNA
; LENGTH: 1749
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-351-348-56

Query Match      61.1%; Score 1011.4; DB 3; Length 1749;
Best Local Similarity 78.9%; Pred. No. 3.5e-213;
Matches 1329; Conservative 0; Mismatches 296; Indels 60; Gaps 8;

QY      1  GATCTATCTACTGACCTTCGCGCAGCGGCGGTACCCGGGTGGCTGAGTACTCGGCG 60
Db      95  GATCTATCTACTGACCTTCGCGCAGCGGCGGTACCCGGGTGGCTGAGTACTCGGCG 154
QY      61  ATCCGCTGGCGACCGCTTCGCGCGTTCGCGAGCATCAACCGCATGGAAGCAAGCATGG 120
Db      155  ATCCGCTGGCGACCGCTTCGCGCGTTCGCGAGCATCAACCGCATGGAAGCAAGCATGG 214
QY      121  TGGCAACCGTCCCGCATTCGCGCAGCAGGTGCTCGGACCGGCTTCGCGCATCTCGCG 180
Db      215  TGGCAACCGTCCCGCATTCGCGCAGCAGGTGCTCGGACCGGCTTCGCGCATCTCGCG 274
QY      181  CCGGCAACCGTTCGCTTCGCGCAGCAGGTGCTCGGACCGGCTTCGCGCATCTCGATC 240
Db      275  CCGGCAACCGTTCGCTTCGCGCAGCAGGTGCTCGGACCGGCTTCGCGCATCTCGATC 334
QY      241  CAGAACCGGCGCGCTTCGCGGTTGAGGTCTCTCGGTGCCAGTTCGCGCATCTCGCG 300
Db      335  CAGAACCGGCGCGCTTCGCGGTTGAGGTCTCTCGGTGCCAGTTCGCGCATCTCGCG 394
QY      301  TCGCGCTGGTGTATGCGCGCGCTTCGCGCATCTCGGTTCGCGCATCTCGCGCGCT 360
Db      395  TCGCGCTGGTGTATGCGCGCGCTTCGCGCATCTCGGTTCGCGCATCTCGCGCGCT 454
QY      361  GCGCGATGATCTATCAGTTCGCGCGCTTCGCGCATCTCGGTTCGCGCATCTCGCG 420
Db      455  GCGCGATGATCTATCAGTTCGCGCGCTTCGCGCATCTCGGTTCGCGCATCTCGCG 510
QY      421  CTCCGCGCTTCGATTCGCGGTTGGGTTCGCGCATCTCGGTTCGCGCATCTCGCG 480
Db      511  TCCAAATGTCTTCAGCAGGATCCGA-----TGCAGAACACCGCACCGCAGCAGT 564
QY      481  GCAACGGGTTCGCGCAGCGGTTCGCGCATCTCTCCAGTTCGCGCATCTCGCGCGCT 540
Db      565  GCAATCTGTCTTCGCGCAGCGGTTCGCGCATCTCTCCAGTTCGCGCATCTCGCGCG 624
QY      541  CCGCGCGCAGCAGCGGTTCGCGCATCTCTCCAGTTCGCGCATCTCGCGCGCT 600
Db      625  GTCCGCGCGCGCGCT-----GCGCGCGCTCTCCATGCGCGGTTGTTCACT 671
QY      601  CGTCGGGCTTCGCGCAGGTTCAGGATCCAGGATCCAGGATCCAGGATCCAGGATCCAG 660

```



QY 661 GCGGGGATCTGATCAGCTCGGGAGCCCGGGTSCCCAGCAACGCCAGCGTGGGAAGCACC 720  
 Db 617 GCGGGGATCTGATC-----GCGAGCATCAAGACAGTAAAGCGGTTCGCGTT 666  
 QY 721 GAGACCGCGGATGTGCGCGCAGCAGCGCCAGCGGTGCAACCCCGGGAGCCCGGCC 780  
 Db 667 GAATCCNATGTGTGTCAGCAGGATCCGATGCGCAACCCGACCGAGCAGTCGCA 726  
 QY 781 CCGCGGACCGGTGCGAGTCGACCCCGCGCCCAACCGCCCGCGCGTGTGTGTCAGCATCAGC 840  
 Db 727 ATCTGTCTCGCACCTCGGCTCAGCGCGGTGCTGCTCGCAACCCCGCGCGATGTC 786  
 QY 841 CAGCGGATGATCTGATCGCAGGC-----ATCAGCAACAGTAAAGCGGTTCGCGTTGAT 897  
 Db 787 GCGCGCGCGCTCGGCGCGCTCTCCATGCGCGGTTCGTTCACTCGCTGTCGCGGTGGCT 846  
 QY 898 CCAATGTGCTGTCAGCAGGATCCGATGCGCAACCCAGCAGCGAGTCGCAATCT 957  
 Db 847 GTTCGGAACGGCGCGCGCGCTGCTGCTCGATAGGGATCTGATCAGCTCGGG 906  
 QY 958 GTCTCGGACCTGTGCGTCAAGCGCGGTGTGCTCGCAACCCCGCGCGATGTGCGCG 1017  
 Db 907 GAGCGCGGTGCCAGCAACCGCAGCGTGGGAACCGAGACCGCGCGATGTGCGCGCG 966  
 QY 1018 GCGCGCTGCGGCGGCTCTCCATGCGCGGTTCGTTCACTCGCTGCTCGGTGGCTGTC 1077  
 Db 967 CAGCAGCGCCAGCGTGCACCCCGCGGACCGCGGCCCGCGAGCCGTCGAGTCGAC 1026  
 QY 1078 TGGCAACGGGCGCGCGCGC-----CGTCGTCCGTCCGATACGGGATCTATCAGCAG 1130  
 Db 1027 CCGGCGCGCACCGCGCGCGGTGTGTCAGCATCAGCCAGCGGATGGAATCTATCAGCAG 1086  
 QY 1131 GTAGGCGCTCCAGCGTACTCTTCGCGCCAGAAACAGCGGTGCGTCCGCGCGCAGACCAG 1190  
 Db 1087 GTAGGCGCTCCAGCGTACTCTTCGCGCCAGAAACAGCGGTGCGTCCGCGCGCAGACCAG 1146  
 QY 1191 CGGTCTCGCGCAGATACACCCAGCGGTGCGCGCATGTCCAGATCGTGGCCAGCGCG 1250  
 Db 1147 CGGTCTCGCGCAGATACACCCAGCGGTGCGCGCATGTCCAGATCGTGGCCAGCGCG 1206  
 QY 1251 CCGGCGACGCTGAGATCGGATCTATCGCGCGCTGTGCGGGAAGACGAGGCGGTAGCG 1310  
 Db 1207 CCGGCGACGCTGAGATCGGATCTATCGCGCGCTGTGCGGGAAGACGAGGCGGTAGCG 1266  
 QY 1311 GCGTTGCACTAGTTCGCGCGGTGCGGGAAGACGAGATCAATCGACGAGCCTTGCGC 1370  
 Db 1267 GCGTTGCACTAGTTCGCGCGGTGCGGGAAGACGAGATCAATCGACGAGCCTTGCGC 1326  
 QY 1371 AACATCGGCGGTATCTGCGCAGCTGAGGTTCCCGCTCTCGTCG----- 1413  
 Db 1327 AACATCGGCGGTATCTGCGCAGCTGAGGTTCCCGCTCTCGTCGATCTGATCAGAACGG 1386  
 QY 1414 ----- 1413  
 Db 1387 GCGGCTCGCGGTTGAGTCTCTCGGTGCCAGTGCCTGCGACGCGACGTCGTGCGGCT 1446  
 QY 1414 ----- 1413  
 Db 1447 GGTGATGCGCGCGCTGAGCGTCTCTCGGTCCAAACGTGACGACCGTGCCTCGGCGGAT 1506  
 QY 1414 -GATCTATCCGCGCACCGCGCGGTGCGCGCACCGCGTGGATCGTTGTCAGTACCGG 1472  
 Db 1507 GGATCTATCCGCGCGCACCGCGCGGTGCGCGCACCGCGTGGATCGTTGTCAGTACCGG 1566  
 QY 1473 AAGCTCTTGAGCTAAGGCAATTTGGGAAGATATTGGACCTTCCCATCAATAGAGGAA 1532  
 Db 1567 AAGCTCTTGAGCTAAGGCAATTTGGGAAGATATTGGACCTTCCCATCAATAGAGGAA 1626  
 QY 1533 AAGCATCGCCTTAGGGATCCGATAGCGGCGCGGTGTTTCAGTGAACCTTGGCGAGGCA 1592  
 Db 1627 AAGCATCGCCTTAGGGATCCGATAGCGGCGCGGTGTTTCAGTGAACCTTGGCGAGGCA 1686

QY 1593 ATCCATCGCGCAGCGCGGAAATCCAGGATCCATCACCATCACCATCACCATC 1652  
 Db 1687 ATCCATCGCGCAGCGCGGAAATCCAGGATCCATCACCATCACCATCACCATC 1746  
 QY 1653 TGA 1655  
 Db 1747 TGA 1749

RESULT 6  
 US-09-351-348-57  
 ; Sequence 57, Application US/09351348  
 ; Patent No. 6436898  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Delcayre, Alain  
 ; TITLE OF INVENTION: Compounds and Methods for the Treatment  
 ; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines  
 ; FILE REFERENCE: 11000.1042  
 ; CURRENT APPLICATION NUMBER: US/09/351,348  
 ; CURRENT FILING DATE: 1999-07-12  
 ; NUMBER OF SEQ ID NOS: 81  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 57  
 ; LENGTH: 1749  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Made in a lab  
 US-09-351-348-57

Query Match 44.7%; Score 740.2; DB 3; Length 1749;  
 Best Local Similarity 69.0%; Pred. No. 1.5e-153;  
 Matches 1244; Conservative 0; Mismatches 263; Indels 296; Gaps 5;

QY 1 GATCTATCTACTCGACCTTCGCCGACCGGGCGTACCCGGTGGCTTCACTCGCGCC 60  
 Db 95 GATCTATCTACTCGACCTTCGCCGACCGGGCGTACCCGGTGGCTTCACTCGCGCC 154  
 QY 61 ATCCGTGCGGACCGCTGCGCGTCCGACCATCAACCGGATGGAGAGGAGCATCG 120  
 Db 155 ATCCGTGCGGACCGCTGCGCGTCCGACCATCAACCGGATGGAGAGGAGCATCG 214  
 QY 121 TGGCCAAACGCTCGCGCATCGCGAGCAGTGTCTCGGACCGGTCTGCGCGATCTCGCG 180  
 Db 215 TGGCCAAACGCTCGCGCATCGCGAGCAGTGTCTCGGACCGGTCTGCGCGATCTCGCG 274  
 QY 181 CCGGCAACGCTTCGCTCGCGGAGTCCGCGCTCGGCGTCTTCGCGGCGGATCTGATC 240  
 Db 275 CCGGCAACGCTTCGCTCGCGGAGTCCGCGCTCGGCGTCTTCGCGGCGG----- 324  
 QY 241 CAGAACGGGCGGCTGCGCGGTTGAGGTCTCTCGGTGCCAGTGCCTGCGACGCGATCG 300  
 Db 325 ----- 324  
 QY 301 TCGGCGCTGCTGATCGGCGCGGTAGGCGTCTCTCGGTCCACAAACGTCAGACCGTGC 360  
 Db 325 ----- 324  
 QY 361 GGGCGGATGGATCTATCAGTTCGCGCTTGGTCCGACCGCGCGGAGGCGAGCTTCG 420  
 Db 325 -----GGATCTATCAGTTCGCGCTTGGTCCGACCGCGCGGAGGCGAGCTTCG 376  
 QY 421 CTCGCGCGTTCGATCGGTTGGTTCGTCGCGGCGGACACACAGCATCCACCGAGTCCA 480  
 Db 377 CTCGCGCGTTCGATCGGTTGGTTCGTCGCGGCGGACACACAGCATCCACCGAGTCCA 436  
 QY 481 GCAACGGGTCGCCGAGTGCATCTCCAGTTCGATGAACCGCGAGCTCGGGGACGT 540  
 Db 437 GCAACGGGTCGCCGAGTGCATCTCCAGTTCGATGAACCGCGAGCTCGGGGACGT 496  
 QY 541 CCGCGCGCAGCAGCAGTTCGATGCGAGTTCGCGGTGATGATCCCGGGTTCGGCGT 600  
 Db 497 CCGCGCGCAGCAGCAGTTCGATGCGAGTTCGCGGTGATGATCCCGGGTTCGGCGT 556

QY 601 CQTGGGCTTGGCGAGTCCAGCAGTCCGCGAGCAGATGACCCAGCGGAAACGACTCCG 660  
Db 557 CTTGGGCTTGGCGAGTCCAGCAGTCCGCGAGCAGATGACCCAGCGGAAACGACTCCG 616  
QY 661 GCGCGGATCTGATCAGCTCGGGAGCCCGGTGCCAGCAACGCCAGCTGGGAAGCACC 720  
Db 617 GCGCGGATCTGATC-----GCGAGGATCAGCAACAGTAAGCGGTGTTCCGGTT 666  
QY 721 GAGACGGCGGATGTCGCCCGCAGCGGCCAGCGGTGACCCCGGGGACCGGCC 780  
Db 667 GATCCAAATGTCGTGTCAGCAGCATCCGATGCCGAACACCGACACCGGAGCAGTCGCA 726  
QY 781 CCGCGGACCGCTCGGAGTGCAGCCCGCGCCGACCGCGCGCGCGTGGTTCAGCATCAGC 840  
Db 727 ATCTGTCTCCGACCCCTCGGCTCAGCGGGTCTGCTGCTCCGGAACCCCGCGGATGTC 786  
QY 841 CACGGATGATCTGATCGCAGGC---ATCAGCAACAGTAAGCGGTGTTCCGGTTGAAT 897  
Db 787 GCGCGCGCGCTCGCGCGGCTCTCCATGCGCGTCTGTTCACTGCTGCTCGGTGGCT 846  
QY 898 CCAATGTGTCAGCAGGATCCGATGCCGAACACCGACACCGGAGCAGTCCGCAATCT 957  
Db 847 GTTCTCGAAGCGGCGCGCGCGCTGCTGCTGCGATACGGGATCTGATCAGCTCGGG 906  
QY 958 GTCTCGGACCTGGGTCAGCGGCGTCTGCTGCTGCGCAACCGCGCGCGATGTCGCGC 1017  
Db 907 GAGCGGGTCCCGAGCAACCGAGCGTGGGAAGCAGCGCGCGGATGTCGCGCG 966  
QY 1018 GCGCGCTCGCGCGGCTCTCCATGCGCGGCTTCTGTTCACTGCTGCTGCTGCGTGGCT 1077  
Db 967 CAGCAGCGCCAGCGGTGCAACCGCGGACCGGCGCGCGCGGATGTCGAGTCGAC 1026  
QY 1078 TGGGAAGCGGCGCGCGCGC-----CGTGTCTCGTCCGATACGGGATCTATCAGCAG 1130  
Db 1027 CCGCGCGCGCAGCGCGCGCGGTGCTCAGCATCAGCCAGCGGATGATCTATCAGCAG 1086  
QY 1131 GTAGGCGCTCCAGCGTACTTTCGCGCCAGAACAGCGGTGCGCGCGCAGACCCAG 1190  
Db 1087 GTAGGCGCTCAGCGGTACTTTCGCGCCAGAACAGCGGTGCGCGCGCAGACCCAG 1146  
QY 1191 CGGTCTTCGCGCGCAGATACACCCAGCGGTGCGCGCATGTCAGATCGTGGCCAGCGG 1250  
Db 1147 CGGTCTTCGCGCGCAGATACACCCAGCGGTGCGCGCATGTCAGATCGTGGCCAGCGG 1206  
QY 1251 CGCGCACGCTGAGATCGGATCTATCGCGCGGTGTCGCGGAAGGACGAGCGCGTAGCG 1310  
Db 1207 CGCGCACGCTGAGATCGGATCTATCGCGCGGTGTCGCGGAAGGACGAGCGCGTAGCG 1266  
QY 1311 GCGTTGCACTACGTCGCGCGGTTGGGAGAGCAGGACTACATCGACCGGAGCTTCGCGC 1370  
Db 1267 GCGTTGCACTACGTCGCGCGGTTGGGAGAGCAGGACTACATCGACCGGAGCTTCGCGC 1326  
QY 1371 AACATCGGCGGTATCTGCGAGCTGAGGTTCCCGCTCTCGTCG----- 1413  
Db 1327 AACATCGGCGGTATCTGCGAGCTGAGGTTCCCGCTCTCGTCGAGATCTGATCCAGACGG 1386  
QY 1414 ----- 1413  
Db 1387 GCGGTCTCGGGTTGAGTCTCTCGGTGCCAGTGCCGTCGACGCGAGCTGTCGCGGCT 1446  
QY 1414 ----- 1413  
Db 1447 GGTGATCGGCGCGGTAGCGTCTCTCGGTCAACAGCTCAGCACCGTGGCCCGCGGAT 1506  
QY 1414 -GATCTATCGCGCACCGCGCGGTGCGCGGACCGCGTGATGCTGTCAGTACCGG 1472  
Db 1507 GATCTATCGCGCACCGCGCGGTGCGCGGACCGCGTGATGCTGTCAGTACCGG 1566  
QY 1473 AAGCTCTTGAGAGTAAGGCGCAATTGGGAAGATATCTTGGACCTTCCCATCAATAGAGAA 1532  
Db 1567 AAGCTCTTGAGAGTAAGGCGCAATTGGGAAGATATCTTGGACCTTCCCATCAATAGAGAA 1626

QY 1533 AAGCATCGCCCTAGGGATCCCTAGCGGGCCCGGTGTTTCGATGTAACTTGGGCGGGCA 1592  
Db 1627 AAGCATCGCCCTAGGGATCCCTAGCGGGCCCGGTGTTTCGATGTAACTTGGGCGGGCA 1686  
QY 1593 ATCCCATCGCGCGCAGCCCGCGGGAATCCACGGATCCATCACCATCACCATCAC 1652  
Db 1687 ATCCCATCGCGCGCAGCCCGCGGGAATCCACGGATCCATCACCATCACCATCAC 1746  
QY 1653 TGA 1655  
Db 1747 TGA 1749

RESULT 7

US-09-450-072-15  
; Sequence 15, Application US/09450072  
; Patent No. 6358734  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder  
; TITLE OF INVENTION: and Methods for Their Use  
; FILE REFERENCE: 11000.1042c1  
; CURRENT APPLICATION NUMBER: US/09/450,072  
; CURRENT FILING DATE: 1999-11-29  
; EARLIER APPLICATION NUMBER: 09/351,348  
; EARLIER FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 291  
; TYPE: DNA  
; ORGANISM: Mycobacterium vaccae  
US-09-450-072-15

Query Match 17.6%; Score 291; DB 3; Length 291;

Best Local Similarity 100.0%; Pred. No. 6.3e-55;  
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 ATCAGTTTCGGCCCTGCTCGCCAGCCCGCGAGGCGAGCCAGTTCCGCTCCGGGTCGATC 434  
Db 1 ATCAGTTTCGGCCCTGCTCGCCAGCCCGCGAGGCGAGCCAGTTCCGCTCCGGGTCGATC 60  
QY 435 GGGTTGGTTCGCTCCGGCCAGCAACACAGCATCCACCGAGGTCGAGCAACGGGTCCCG 494  
Db 61 GGGTTGGTTCGCTCCGGCCAGCAACACAGCATCCACCGAGGTCGAGCAACGGGTCCCG 120  
QY 495 ACGGTGCACATCTCCAGTCGATGAACGCGCGAGCTCGGGAGCTCGCGCGCAGCAGC 554  
Db 121 ACGGTGCACATCTCCAGTCGATGAACGCGCGAGCTCGGGAGCTCGCGCGCAGCAGC 180  
QY 555 ACGTTGTCAGATGGCAGTCGCGGTGATGATCCCGGTTTCGGGCTCGTCCGGCTCGCG 614  
Db 181 ACGTTGTCAGATGGCAGTCGCGGTGATGATCCCGGTTTCGGGCTCGTCCGGCTCGCG 240  
QY 615 GAGTCCAGCCAGTCGCGGAGCAGCATGACCCAGCGGAAACGACTCGGGCGCG 665  
Db 241 GAGTCCAGCCAGTCGCGGAGCAGCATGACCCAGCGGAAACGACTCGGGCGCG 291

RESULT 8

US-09-351-348-15  
; Sequence 15, Application US/09351348  
; Patent No. 643698  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines  
; FILE REFERENCE: 11000.1042  
; CURRENT APPLICATION NUMBER: US/09/351,348  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15

```
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-351-348-15

Query Match      17.6%; Score 291; DB 3; Length 291;
Best Local Similarity 100.0%; Pred. No. 6.3e-55;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 ATCAGTTGCGCCTGTGTCGACCGCCGAGGCGACGATTCCTCGGCGTGCATC 434
    |||
Db 1 ATCAGTTGCGCCTGTGTCGACCGCCGAGGCGACGATTCCTCGGCGTGCATC 60

QY 435 GGGTTGGGTCGTCGCGGCGACACACGACGATCCACCGGAGTTCGAGCAACGGTCCCCG 494
    |||
Db 61 GGGTTGGGTCGTCGCGGCGACACACGACGATCCACCGGAGTTCGAGCAACGGTCCCCG 120

495 ACGGTGCACATCTCCAGTCGATGAACCGCCGCGAGCTCGGGGACGTTCGGGCGCAGCAGC 554
    |||
Db 121 ACGGTGCACATCTCCAGTCGATGAACCGCCGCGAGCTCGGGGACGTTCGGGCGCAGCAGC 180

QY 555 ACCTTTGTCAGATGGCAGTCGCGTGCATGATCCCGGGTTTCGGCGTCGTTCGGGCGTGGCG 614
    |||
Db 181 ACCTTTGTCAGATGGCAGTCGCGTGCATGATCCCGGGTTTCGGCGTCGTTCGGGCGTGGCG 240

QY 615 GAGTCCAGCCAGTCGGCGAGCACATGCACCGAGGGAACGACTCGGGGCGG 665
    |||
Db 241 GAGTCCAGCCAGTCGGCGAGCACATGCACCGAGGGAACGACTCGGGGCGG 291

RESULT 9
US-09-450-072-18
; Sequence 18, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-450-072-18

Query Match      15.8%; Score 261; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.4e-48;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 GATCGCGAGGCATCACGAACAGTAAGCGGTGTTCGGTTGAATCCAAATGCTGTGCAGCA 914
    |||
Db 1 GATCGCGAGGCATCACGAACAGTAAGCGGTGTTCGGTTGAATCCAAATGCTGTGCAGCA 60

QY 915 GGCATCCGATGCCGAACACCGACCGAGCAGTGCCTCGCGCGCGCGCGCGCGCGCG 974
    |||
Db 61 GGCATCCGATGCCGAACACCGACCGAGCAGTGCCTCGCGCGCGCGCGCGCGCGCGCG 120

QY 975 TCACGCGCGCGTGTGGTCTCCGCAACCCCGCGCGCGATGTCGCGCGCGCGCGCGCGCG 1034
    |||
Db 121 TCACGCGCGCGTGTGGTCTCCGCAACCCCGCGCGCGATGTCGCGCGCGCGCGCGCGCG 180

QY 1035 TCTCCATGCGCGGTTCGTTCAAGTCGCTCGTTCGGTGGCTGTCTCGGAACGGGCGCGCG 1094
    |||
Db 181 TCTCCATGCGCGGTTCGTTCAAGTCGCTCGTTCGGTGGCTGTCTCGGAACGGGCGCGCG 240

QY 1095 CCCCCTCGTCCGTCGCGATACG 1115
    |||
Db 241 CCCCCTCGTCCGTCGCGATACG 261

RESULT 11
US-09-450-072-14
; Sequence 14, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 697
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-450-072-14

Query Match      13.7%; Score 226; DB 3; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.5e-40;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATCTACTCGACCTTCGCGCGCGGTACCCGCGGTGGCTGACGTACTCTCGGCGCATCCG 65
```

```
Db 241 CCCCCTCGTCCGTCGCGATACG 261

RESULT 10
US-09-351-348-18
; Sequence 18, Application US/09351348
; Patent No. 6436898
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines
; FILE REFERENCE: 11000.1042
; CURRENT APPLICATION NUMBER: US/09/351,348
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-351-348-18

Query Match      15.8%; Score 261; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.4e-48;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 GATCGCGAGGCATCACGAACAGTAAGCGGTGTTCGGTTGAATCCAAATGCTGTGCAGCA 914
    |||
Db 1 GATCGCGAGGCATCACGAACAGTAAGCGGTGTTCGGTTGAATCCAAATGCTGTGCAGCA 60

QY 915 GGCATCCGATGCCGAACACCGACCGAGCAGTGCCTCGCGCGCGCGCGCGCGCGCG 974
    |||
Db 61 GGCATCCGATGCCGAACACCGACCGAGCAGTGCCTCGCGCGCGCGCGCGCGCGCGCG 120

QY 975 TCACGCGCGCGTGTGGTCTCCGCAACCCCGCGCGCGATGTCGCGCGCGCGCGCGCGCG 1034
    |||
Db 121 TCACGCGCGCGTGTGGTCTCCGCAACCCCGCGCGCGATGTCGCGCGCGCGCGCGCGCG 180

QY 1035 TCTCCATGCGCGGTTCGTTCAAGTCGCTCGTTCGGTGGCTGTCTCGGAACGGGCGCGCG 1094
    |||
Db 181 TCTCCATGCGCGGTTCGTTCAAGTCGCTCGTTCGGTGGCTGTCTCGGAACGGGCGCGCG 240

QY 1095 CCCCCTCGTCCGTCGCGATACG 1115
    |||
Db 241 CCCCCTCGTCCGTCGCGATACG 261

RESULT 11
US-09-450-072-14
; Sequence 14, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 697
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-450-072-14

Query Match      13.7%; Score 226; DB 3; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.5e-40;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATCTACTCGACCTTCGCGCGCGGTACCCGCGGTGGCTGACGTACTCTCGGCGCATCCG 65
```

Db 1 ATCTACTCGACCTTCGCGGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 60  
Qy 66 CTGGCGACCGCCTTCGGCGGTTCGGACGATCAACGCGGATGGAAGACGAGGCATGTGGCC 125  
Db 61 CTGGCGACCGCCTTCGGCGGTTCGGACGATCAACGCGGATGGAAGACGAGGCATGTGGCC 120  
Qy 126 AACGCTGCCCGCATCGCGGACGAGGTGCTCGGACCGGGTCTGCGCGATCTCGCGCCCGG 185  
Db 121 AACGCTGCCCGCATCGCGGACGAGGTGCTCGGACCGGGTCTGCGCGATCTCGCGCCCGG 180  
Qy 186 CACCGTTTCGGTTCGGCGAAGTTCGGCGCTTCGGGGTCTTCTGGGGCGG 231  
Db 181 CACCGTTTCGGTTCGGCGAAGTTCGGCGCTTCGGGGTCTTCTGGGGCGG 226

RESULT 12  
US-09-351-348-14  
; Sequence 14, Application US/09351348  
; Patent No. 6436898  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines  
; FILE REFERENCE: 11000.1042  
; CURRENT APPLICATION NUMBER: US/09/351,348  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 697  
; TYPE: DNA  
; ORGANISM: Mycobacterium vaccae  
US-09-351-348-14

Query Match 13.7%; Score 226; DB 3; Length 697;  
Best Local Similarity 100.0%; Pred. No. 1.5e-40;  
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 ATCTACTCGACCTTCGCGGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 65  
Db 1 ATCTACTCGACCTTCGCGGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 60  
Qy 66 CTGGCGACCGCCTTCGGCGGTTCGGACGATCAACGCGGATGGAAGACGAGGCATGTGGCC 125  
Db 61 CTGGCGACCGCCTTCGGCGGTTCGGACGATCAACGCGGATGGAAGACGAGGCATGTGGCC 120  
Qy 126 AACGCTGCCCGCATCGCGGACGAGGTGCTCGGACCGGGTCTGCGCGATCTCGCGCCCGG 185  
Db 121 AACGCTGCCCGCATCGCGGACGAGGTGCTCGGACCGGGTCTGCGCGATCTCGCGCCCGG 180  
Qy 186 CACCGTTTCGGTTCGGCGAAGTTCGGCGCTTCGGGGTCTTCTGGGGCGG 231  
Db 181 CACCGTTTCGGTTCGGCGAAGTTCGGCGCTTCGGGGTCTTCTGGGGCGG 226

RESULT 13  
US-09-450-072-13  
; Sequence 13, Application US/09450072  
; Patent No. 6358734  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; TITLE OF INVENTION: and Methods for Their Use  
; FILE REFERENCE: 11000.1042c1  
; CURRENT APPLICATION NUMBER: US/09/450,072  
; CURRENT FILING DATE: 1999-11-29  
; EARLIER APPLICATION NUMBER: 09/351,348  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 210

; TYPE: DNA  
; ORGANISM: Mycobacterium vaccae  
US-09-450-072-13  
Query Match 12.7%; Score 210; DB 3; Length 210;  
Best Local Similarity 100.0%; Pred. No. 3.8e-37;  
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1419 ATCGCGCCACCGCGCGGTGCCCGCACCGGTGGATCGTTCGTCACTACCCGAAAGCTC 1478  
Db 1 ATCGCGCCACCGCGCGGTGCCCGCACCGGTGGATCGTTCGTCACTACCCGAAAGCTC 60  
Qy 1479 TTGAGAGCTAAGGCCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGAGGAAAGCAT 1538  
Db 61 TTGAGAGCTAAGGCCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGAGGAAAGCAT 120  
Qy 1539 CGCCCTAGGGGATCCGTAGCGGGCCGGTTCGTGAGTGAACTTGGGCGAGGGCAATCCCA 1598  
Db 121 CGCCCTAGGGGATCCGTAGCGGGCCGGTTCGTGAGTGAACTTGGGCGAGGGCAATCCCA 180  
Qy 1599 TCGCGCGCAGCCCGCGCAGCGGAAATCCAC 1628  
Db 181 TCGCGCGCAGCCCGCGCAGCGGAAATCCAC 210

RESULT 14  
US-09-351-348-13  
; Sequence 13, Application US/09351348  
; Patent No. 6436898  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines  
; FILE REFERENCE: 11000.1042  
; CURRENT APPLICATION NUMBER: US/09/351,348  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 210  
; TYPE: DNA  
; ORGANISM: Mycobacterium vaccae  
US-09-351-348-13

Query Match 12.7%; Score 210; DB 3; Length 210;  
Best Local Similarity 100.0%; Pred. No. 3.8e-37;  
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1419 ATCGCGCCACCGCGCGGTGCCCGCACCGGTGGATCGTTCGTCACTACCCGAAAGCTC 1478  
Db 1 ATCGCGCCACCGCGCGGTGCCCGCACCGGTGGATCGTTCGTCACTACCCGAAAGCTC 60  
Qy 1479 TTGAGAGCTAAGGCCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGAGGAAAGCAT 1538  
Db 61 TTGAGAGCTAAGGCCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGAGGAAAGCAT 120  
Qy 1539 CGCCCTAGGGGATCCGTAGCGGGCCGGTTCGTGAGTGAACTTGGGCGAGGGCAATCCCA 1598  
Db 121 CGCCCTAGGGGATCCGTAGCGGGCCGGTTCGTGAGTGAACTTGGGCGAGGGCAATCCCA 180  
Qy 1599 TCGCGCGCAGCCCGCGCAGCGGAAATCCAC 1628  
Db 181 TCGCGCGCAGCCCGCGCAGCGGAAATCCAC 210

RESULT 15  
US-09-450-072-21  
; Sequence 21, Application US/09450072  
; Patent No. 6358734  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; TITLE OF INVENTION: and Methods for Their Use

; FILE REFERENCE: 11000.1042c1  
; CURRENT APPLICATION NUMBER: US/09/450,072  
; CURRENT FILING DATE: 1999-11-29  
; EARLIER APPLICATION NUMBER: 09/351,348  
; EARLIER FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 177  
; TYPE: DNA  
; ORGANISM: Mycobacterium vaccae  
US-09-450-072-21

Query Match 10.7%; Score 177; DB 3; Length 177;  
Best Local Similarity 100.0%; Pred.No. 6.7e-30;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
672 GATCAGCTCGGGAGCGGGTGCCAGCAAGCCAGCGTGCGGAAGCACCGAGACCGCGC 731  
|||  
1 GATCAGCTCGGGAGCGGGTGCCAGCAAGCCAGCGTGCGGAAGCACCGAGACCGCGC 60  
  
732 GATGTGCCCCCGCAGCAGCGCCCGAGCGGTGCAACCCCGCGGACCCGGGCCCCCGCGGACCGC 791  
|||  
61 GATGTGCCCCCGCAGCAGCGCCCGAGCGGTGCAACCCCGCGGACCCGGGCCCCCGCGGACCGC 120  
  
792 GTCGGAGTCGACCCCGGCGCCGACCGCGCGCGTGGTCAGCATCAGCCACGGGAT 848  
|||  
121 GTCGGAGTCGACCCCGGCGCCGACCGCGCGCGTGGTCAGCATCAGCCACGGGAT 177

Search completed: October 7, 2005, 00:30:42  
Job time : 316 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2005, 20:35:08 ; Search time 171 Seconds  
(without alignments)  
1300.031 Million cell updates/sec

Title: US-10-607-752-116  
Perfect score: 2862  
Sequence: 1 IYSTFADRAYPGLTSGHP.....IPSRARAAEIHGSHHHHH 549

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0  
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09E\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10F\_PUBCOMB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2862	100.0	549	15	US-10-607-752-116
2	2862	100.0	582	14	US-10-100-679-81
3	2862	100.0	582	15	US-10-607-752-81
4	2804	98.0	541	14	US-10-100-679-97
5	2804	98.0	541	15	US-10-607-752-97
6	2431	84.9	471	14	US-10-100-679-96
7	2431	84.9	471	15	US-10-607-752-96
8	2184	76.3	423	14	US-10-100-679-95
9	2184	76.3	423	15	US-10-607-752-95
10	2145	74.9	582	14	US-10-100-679-80
11	2145	74.9	582	15	US-10-607-752-80

12	1919	67.1	372	14	US-10-100-679-94	Sequence 94, Appl
13	1919	67.1	372	15	US-10-607-752-94	Sequence 94, Appl
14	1906	66.6	582	14	US-10-100-679-79	Sequence 79, Appl
15	1906	66.6	582	15	US-10-607-752-79	Sequence 79, Appl
16	1459	51.0	281	14	US-10-100-679-93	Sequence 93, Appl
17	1459	51.0	281	15	US-10-607-752-93	Sequence 93, Appl
18	1123	39.2	220	14	US-10-100-679-92	Sequence 92, Appl
19	1123	39.2	220	15	US-10-607-752-92	Sequence 92, Appl
20	623	21.8	121	14	US-10-100-679-91	Sequence 91, Appl
21	623	21.8	121	15	US-10-607-752-91	Sequence 91, Appl
22	490	17.1	97	14	US-10-100-679-71	Sequence 71, Appl
23	490	17.1	97	15	US-10-607-752-71	Sequence 71, Appl
24	440	15.4	87	14	US-10-100-679-74	Sequence 74, Appl
25	440	15.4	87	15	US-10-607-752-74	Sequence 74, Appl
26	389	13.6	75	14	US-10-100-679-70	Sequence 70, Appl
27	389	13.6	75	15	US-10-607-752-70	Sequence 70, Appl
28	389	13.6	75	15	US-10-607-752-70	Sequence 70, Appl
29	389	13.6	75	15	US-10-607-752-70	Sequence 70, Appl
30	373	13.0	70	14	US-10-100-679-69	Sequence 69, Appl
31	373	13.0	70	15	US-10-607-752-69	Sequence 69, Appl
32	326	11.4	59	14	US-10-100-679-77	Sequence 77, Appl
33	326	11.4	59	15	US-10-607-752-77	Sequence 77, Appl
34	284	9.9	451	14	US-10-156-761-12085	Sequence 12085, A
35	255	8.9	49	14	US-10-100-679-72	Sequence 72, Appl
36	255	8.9	49	15	US-10-607-752-72	Sequence 72, Appl
37	237	8.3	46	14	US-10-100-679-73	Sequence 73, Appl
38	237	8.3	46	15	US-10-607-752-73	Sequence 73, Appl
39	224	7.8	44	14	US-10-100-679-76	Sequence 76, Appl
40	224	7.8	44	15	US-10-607-752-76	Sequence 76, Appl
41	220	7.7	445	9	US-09-815-242-11701	Sequence 11701, A
42	206	7.2	38	14	US-10-100-679-67	Sequence 67, Appl
43	206	7.2	38	15	US-10-607-752-67	Sequence 67, Appl
44	203.5	7.1	19608	15	US-10-084-846A-8	Sequence 8, Appl
45	197.5	6.9	900	18	US-10-450-763-33892	Sequence 33892, A

ALIGNMENTS

RESULT 1  
US-10-607-752-116  
; Sequence 116, Application US/10607752  
; Publication No. US2004007224A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder:  
; FILE REFERENCE: 11000.1042c3  
; CURRENT APPLICATION NUMBER: US/10/607,752  
; PRIOR FILING DATE: 2003-06-26  
; PRIOR APPLICATION NUMBER: 10/100,679  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 08/351,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 116  
; LENGTH: 549  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-10-607-752-116

Query Match 100.0% Score 2862; DB 15; Length 549;  
Best Local Similarity 100.0%; Pred.No. 3.6e-137;  
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IYSTFADRAYPGLTSGHPPLATACAVATINAMEDGVNNAARIGEQVLGFLDLAAR 60  
DB 1 IYSTFADRAYPGLTSGHPPLATACAVATINAMEDGVNNAARIGEQVLGFLDLAAR 60

QY 61 HRSVGEVRLGLVFWAGSDPERAGLVEVLGAQCRRRDVVGAGDAAAVGLGPGQHRARA 120  
DB 61 HRSVGEVRLGLVFWAGSDPERAGLVEVLGAQCRRRDVVGAGDAAAVGLGPGQHRARA 120  
QY 121 DGSISALVASPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
DB 121 DGSISALVASPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
QY 181 RSSTLFRWQSPCMIWPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKHRD 240  
DB 181 RSSTLFRWQSPCMIWPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKHRD 240  
QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGOHQPRDGSROASRTVSGVPPVESNV 300  
DB 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGOHQPRDGSROASRTVSGVPPVESNV 300  
QY 301 LSAGIRCRPTTTRAVAICLATLASGVVAPAGDVVARAAAAGSPWPVRSVARPVAVLRT 360  
DB 301 LSAGIRCRPTTTRAVAICLATLASGVVAPAGDVVARAAAAGSPWPVRSVARPVAVLRT 360  
QY 361 GPPRRPSDTGSIITQVGRPAVLFAPEQRCRRRADORSCQRIHPGGGRHVQIVASARGTVE 420  
DB 361 GPPRRPSDTGSIITQVGRPAVLFAPEQRCRRRADORSCQRIHPGGGRHVQIVASARGTVE 420  
QY 421 IGSIRARLCKDEAVAAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480  
DB 421 IGSIRARLCKDEAVAAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480  
QY 481 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 540  
DB 481 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 540  
QY 541 HGSHHHHH 549  
DB 541 HGSHHHHH 549

RESULT 2  
US-10-100-679-81  
; Sequence 81, Application US/101006759  
; Publication No. US20030054013A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; FILE REFERENCE: 11000.1042c2  
; CURRENT APPLICATION NUMBER: US/10/100,679  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1998-11-29  
; PRIOR APPLICATION NUMBER: 09/361,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 81  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-10-100-679-81

Query Match 100.0%; Score 2862; DB 14; Length 582;  
Best Local Similarity 100.0%; Pred. No. 3.9e-197;  
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60  
DB 34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 93

QY 61 HRSVGEVRLGLVFWAGSDPERAGLVEVLGAQCRRRDVVGAGDAAAVGLGPGQHRARA 120  
DB 94 HRSVGEVRLGLVFWAGSDPERAGLVEVLGAQCRRRDVVGAGDAAAVGLGPGQHRARA 153  
QY 121 DGSISALVASPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
DB 154 DGSISALVASPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 213  
QY 181 RSSTLFRWQSPCMIWPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKHRD 240  
DB 214 RSSTLFRWQSPCMIWPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKHRD 273  
QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGOHQPRDGSROASRTVSGVPPVESNV 300  
DB 274 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGOHQPRDGSROASRTVSGVPPVESNV 333  
QY 301 LSAGIRCRPTTTRAVAICLATLASGVVAPAGDVVARAAAAGSPWPVRSVARPVAVLRT 360  
DB 334 LSAGIRCRPTTTRAVAICLATLASGVVAPAGDVVARAAAAGSPWPVRSVARPVAVLRT 393  
QY 361 GPPRRPSDTGSIITQVGRPAVLFAPEQRCRRRADORSCQRIHPGGGRHVQIVASARGTVE 420  
DB 394 GPPRRPSDTGSIITQVGRPAVLFAPEQRCRRRADORSCQRIHPGGGRHVQIVASARGTVE 453  
QY 421 IGSIRARLCKDEAVAAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480  
DB 454 IGSIRARLCKDEAVAAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 513  
QY 481 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 540  
DB 514 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 573  
QY 541 HGSHHHHH 549  
DB 574 HGSHHHHH 582

RESULT 3  
US-10-607-752-81  
; Sequence 81, Application US/10607752  
; Publication No. US20040072224A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; FILE REFERENCE: 11000.1042c3  
; CURRENT APPLICATION NUMBER: US/10/607,752  
; CURRENT FILING DATE: 2003-06-26  
; PRIOR FILING DATE: 2003-06-26  
; PRIOR APPLICATION NUMBER: 10/100,679  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1998-11-29  
; PRIOR APPLICATION NUMBER: 09/361,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 81  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-10-607-752-81

Query Match 100.0%; Score 2862; DB 15; Length 582;  
Best Local Similarity 100.0%; Pred. No. 3.9e-197;  
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60  
DB 34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 93  
QY 61 HRSVGEVRLGLVFWAGSDPERAGLVEVLGAQCRRRDVVGAGDAAAVGLGPGQHRARA 120

Db 94 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGPGQRHARA 153  
|  
Qy 121 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
|  
Db 154 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 213  
|  
Qy 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGCEGPAQQRORQKRD 240  
|  
Db 214 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGCEGPAQQRORQKRD 273  
|  
Qy 241 RDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHQPDRGSDRQASRTVSGVPVSNV 300  
|  
Db 274 RDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHQPDRGSDRQASRTVSGVPVSNV 333  
|  
Qy 301 LSAGIRCRPTTTRAVAI CLATLASGVVAPQAGDVARAAAAGSPWPVRSVARPVAVLRT 360  
|  
Db 334 LSAGIRCRPTTTRAVAI CLATLASGVVAPQAGDVARAAAAGSPWPVRSVARPVAVLRT 393  
|  
Qy 361 GPPRRPSDTGSI TQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVOIVASARGTVE 420  
|  
Db 394 GPPRRPSDTGSI TQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVOIVASARGTVE 453  
|  
Qy 421 IGSIALRCGKDEAVALHYVAPVGEKQYIDRALRNI GPYLPALVGSIAATGPVPG 480  
|  
Db 454 IGSIALRCGKDEAVALHYVAPVGEKQYIDRALRNI GPYLPALVGSIAATGPVPG 513  
|  
Qy 481 TAWIVRQYPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVRVNLGRAIPRAARAARI 540  
|  
Db 514 TAWIVRQYPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVRVNLGRAIPRAARAARI 573  
|  
Qy 541 HGSHHHHH 549  
|  
Db 574 HGSHHHHH 582  
|

## RESULT 4

US-10-100-679-97  
; Sequence 97, Application US/10100679  
; Publication No. US20030054013A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; FILE REFERENCE: 11000.10422  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: 09/450.072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/451.348  
; PRIOR FILING DATE: 1999-07-12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Mycobacterium vaccae  
US-10-100-679-97

Query Match 98.0%; Score 2804; DB 14; Length 541;  
Best Local Similarity 100.0%; Pred. No. 5.2e-193;  
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEVLGPLEDLAAR 60  
|  
Db 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEVLGPLEDLAAR 60  
|  
Qy 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGPGQRHARA 120  
|  
Db 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGPGQRHARA 120  
|

Qy 121 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
|  
Db 121 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
|  
Qy 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGCEGPAQQRORQKRD 240  
|  
Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGCEGPAQQRORQKRD 240  
|  
Qy 241 RDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHQPDRGSDRQASRTVSGVPVSNV 300  
|  
Db 241 RDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHQPDRGSDRQASRTVSGVPVSNV 300  
|  
Qy 301 LSAGIRCRPTTTRAVAI CLATLASGVVAPQAGDVARAAAAGSPWPVRSVARPVAVLRT 360  
|  
Db 301 LSAGIRCRPTTTRAVAI CLATLASGVVAPQAGDVARAAAAGSPWPVRSVARPVAVLRT 360  
|  
Qy 361 GPPRRPSDTGSI TQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVOIVASARGTVE 420  
|  
Db 361 GPPRRPSDTGSI TQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVOIVASARGTVE 420  
|  
Qy 421 IGSIALRCGKDEAVALHYVAPVGEKQYIDRALRNI GPYLPALVGSIAATGPVPG 480  
|  
Db 421 IGSIALRCGKDEAVALHYVAPVGEKQYIDRALRNI GPYLPALVGSIAATGPVPG 480  
|  
Qy 481 TAWIVRQYPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVRVNLGRAIPRAARAARI 540  
|  
Db 481 TAWIVRQYPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVRVNLGRAIPRAARAARI 540  
|  
Qy 541 H 541  
|  
Db 541 H 541  
|

## RESULT 5

US-10-607-752-97  
; Sequence 97, Application US/10607752  
; Publication No. US2004007224A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; FILE REFERENCE: 11000.1042c3  
; CURRENT FILING DATE: 2003-06-26  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 09/450.072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/451.348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 541  
; TYPE: PRT  
; ORGANISM: Mycobacterium vaccae  
US-10-607-752-97

Query Match 98.0%; Score 2804; DB 15; Length 541;  
Best Local Similarity 100.0%; Pred. No. 5.2e-193;  
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEVLGPLEDLAAR 60  
|  
Db 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEVLGPLEDLAAR 60  
|  
Qy 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGPGQRHARA 120  
|  
Db 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGPGQRHARA 120  
|  
Qy 121 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
|  
Db 121 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
|

```
QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
QY 241 RRDVPAQORPAVHPAGPAGPADRVGVDPGRHRRARGQHOPRDSGDRQASRTVSGVPVESNV 300
Db 241 RRDVPAQORPAVHPAGPAGPADRVGVDPGRHRRARGQHOPRDSGDRQASRTVSGVPVESNV 300
QY 301 LSAGIRCRTPTTTRAVAICLATLASRGVVAPOPAGDVARAAAAGSPWPVRSVARPVAVLRT 360
Db 301 LSAGIRCRTPTTTRAVAICLATLASRGVVAPOPAGDVARAAAAGSPWPVRSVARPVAVLRT 360
QY 361 GPPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGGRHVQIVASARGTVE 420
Db 361 GPPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGGRHVQIVASARGTVE 420
421 IGSIARLCCKDEAAVAALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
Db 421 IGSIARLCCKDEAAVAALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
QY 481 TAWIVROYPKLLARAKANWEDTWTFFSIEKHPRGSGVAGPVRVNLGRAIPSRARAARAEI 540
Db 481 TAWIVROYPKLLARAKANWEDTWTFFSIEKHPRGSGVAGPVRVNLGRAIPSRARAARAEI 540
QY 541 H 541
Db 541 H 541

RESULT 6
US-10-100-679-96
; Sequence 96, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c2
; CURRENT FILING DATE: 2002-03-14
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-100-679-96

Query Match 84.9%; Score 2431; DB 14; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.8e-166;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
Db 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
QY 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAAAGVGLGPQORHARA 120
Db 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAAAGVGLGPQORHARA 120
QY 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
Db 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
QY 241 RRDVPAQORPAVHPAGPAGPADRVGVDPGRHRRARGQHOPRDSGDRQASRTVSGVPVESNV 300
Db 241 RRDVPAQORPAVHPAGPAGPADRVGVDPGRHRRARGQHOPRDSGDRQASRTVSGVPVESNV 300
QY 301 LSAGIRCRTPTTTRAVAICLATLASRGVVAPOPAGDVARAAAAGSPWPVRSVARPVAVLRT 360
Db 301 LSAGIRCRTPTTTRAVAICLATLASRGVVAPOPAGDVARAAAAGSPWPVRSVARPVAVLRT 360
QY 361 GPPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGGRHVQIVASARGTVE 420
Db 361 GPPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGGRHVQIVASARGTVE 420
421 IGSIARLCCKDEAAVAALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
Db 421 IGSIARLCCKDEAAVAALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
QY 481 TAWIVROYPKLLARAKANWEDTWTFFSIEKHPRGSGVAGPVRVNLGRAIPSRARAARAEI 540
Db 481 TAWIVROYPKLLARAKANWEDTWTFFSIEKHPRGSGVAGPVRVNLGRAIPSRARAARAEI 540
QY 541 H 541
Db 541 H 541

RESULT 7
US-10-607-752-96
; Sequence 96, Application US/10607752
; Publication No. US2004007222A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c3
; CURRENT FILING DATE: 2003-06-26
; PRIOR FILING DATE: 2003-06-26
; PRIOR FILING DATE: 2002-03-14
; PRIOR FILING DATE: 1999-11-29
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-607-752-96

Query Match 84.9%; Score 2431; DB 15; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.8e-166;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
Db 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
QY 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAAAGVGLGPQORHARA 120
Db 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAAAGVGLGPQORHARA 120
QY 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
Db 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
QY 241 RRDVPAQORPAVHPAGPAGPADRVGVDPGRHRRARGQHOPRDSGDRQASRTVSGVPVESNV 300
Db 241 RRDVPAQORPAVHPAGPAGPADRVGVDPGRHRRARGQHOPRDSGDRQASRTVSGVPVESNV 300
QY 301 LSAGIRCRTPTTTRAVAICLATLASRGVVAPOPAGDVARAAAAGSPWPVRSVARPVAVLRT 360
Db 301 LSAGIRCRTPTTTRAVAICLATLASRGVVAPOPAGDVARAAAAGSPWPVRSVARPVAVLRT 360
QY 361 GPPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGGRHVQIVASARGTVE 420
Db 361 GPPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGGRHVQIVASARGTVE 420
```

```
Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
QY 241 RRDVPAQORPAVHPAGPAGPADRVGVDPGRHRRARGQHOPRDSGDRQASRTVSGVPVESNV 300
Db 241 RRDVPAQORPAVHPAGPAGPADRVGVDPGRHRRARGQHOPRDSGDRQASRTVSGVPVESNV 300
QY 301 LSAGIRCRTPTTTRAVAICLATLASRGVVAPOPAGDVARAAAAGSPWPVRSVARPVAVLRT 360
Db 301 LSAGIRCRTPTTTRAVAICLATLASRGVVAPOPAGDVARAAAAGSPWPVRSVARPVAVLRT 360
QY 361 GPPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGGRHVQIVASARGTVE 420
Db 361 GPPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGGRHVQIVASARGTVE 420
421 IGSIARLCCKDEAAVAALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALVGS 471
Db 421 IGSIARLCCKDEAAVAALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALVGS 471

RESULT 7
US-10-607-752-96
; Sequence 96, Application US/10607752
; Publication No. US2004007222A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c3
; CURRENT FILING DATE: 2003-06-26
; PRIOR FILING DATE: 2003-06-26
; PRIOR FILING DATE: 2002-03-14
; PRIOR FILING DATE: 1999-11-29
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-607-752-96

Query Match 84.9%; Score 2431; DB 15; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.8e-166;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
Db 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
QY 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAAAGVGLGPQORHARA 120
Db 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAAAGVGLGPQORHARA 120
QY 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
Db 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
QY 241 RRDVPAQORPAVHPAGPAGPADRVGVDPGRHRRARGQHOPRDSGDRQASRTVSGVPVESNV 300
Db 241 RRDVPAQORPAVHPAGPAGPADRVGVDPGRHRRARGQHOPRDSGDRQASRTVSGVPVESNV 300
QY 301 LSAGIRCRTPTTTRAVAICLATLASRGVVAPOPAGDVARAAAAGSPWPVRSVARPVAVLRT 360
Db 301 LSAGIRCRTPTTTRAVAICLATLASRGVVAPOPAGDVARAAAAGSPWPVRSVARPVAVLRT 360
QY 361 GPPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGGRHVQIVASARGTVE 420
Db 361 GPPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGGRHVQIVASARGTVE 420
```

Db 361 GPPRRPDSITQVGRPAVLFAPEQRCRRRADORSCRQIHPPGGRHVQIVASARGTVE 420  
QY 421 IGSIALRCCKDEAAVHVPVGEKQDYIDRALRNIGPVLPAEVPALVGS 471  
Db 421 IGSIALRCCKDEAAVHVPVGEKQDYIDRALRNIGPVLPAEVPALVGS 471

RESULT 8  
US-10-100-679-95  
; Sequence 95, Application US/10100679  
; Publication No. US20030054013A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; FILE REFERENCE: 11000.1042c2  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/351,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 95  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Mycobacterium vaccae  
US-10-100-679-95

Query Match 76.3%; Score 2184; DB 14; Length 423;  
Best Local Similarity 100.0%; Pred. No. 1.4e-148;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTPADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60  
Db 1 IYSTPADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60  
QY 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGQROHRARA 120  
Db 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGQROHRARA 120  
QY 121 DGSISALVAPPPRAASSAPASIGLPGSQHTSIHPRSSNGSPPTVHISQSMNAASSGTSR 180  
Db 121 DGSISALVAPPPRAASSAPASIGLPGSQHTSIHPRSSNGSPPTVHISQSMNAASSGTSR 180  
QY 181 RSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQGEPAQORQKHRD 240  
Db 181 RSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQGEPAQORQKHRD 240  
QY 241 RDVPAQQRPAVHPAGPGPADRVGDPGRHRRARGOHQPRDGSQASRTVSGVPVSNV 300  
Db 241 RDVPAQQRPAVHPAGPGPADRVGDPGRHRRARGOHQPRDGSQASRTVSGVPVSNV 300  
QY 301 LSAGIRCRPTTTRAVAICLAATLASRGVVAQPGDVAAAAAGSPWPVRSVARPVAVLRT 360  
Db 301 LSAGIRCRPTTTRAVAICLAATLASRGVVAQPGDVAAAAAGSPWPVRSVARPVAVLRT 360  
QY 361 GPPRRPDSITQVGRPAVLFAPEQRCRRRADORSCRQIHPPGGRHVQIVASARGTVE 420  
Db 361 GPPRRPDSITQVGRPAVLFAPEQRCRRRADORSCRQIHPPGGRHVQIVASARGTVE 420  
QY 421 IGS 423  
Db 421 IGS 423

RESULT 9  
US-10-607-752-95  
; Sequence 95, Application US/10607752

; Publication No. US20040072224A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder  
; FILE REFERENCE: 11000.1042c3  
; CURRENT FILING DATE: 2003-06-26  
; PRIOR APPLICATION NUMBER: US/10/607,752  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 09/450,072  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/351,348  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 95  
; LENGTH: 423  
; TYPE: PRT  
; ORGANISM: Mycobacterium vaccae  
US-10-607-752-95

Query Match 76.3%; Score 2184; DB 15; Length 423;  
Best Local Similarity 100.0%; Pred. No. 1.4e-148;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTPADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60  
Db 1 IYSTPADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60  
QY 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGQROHRARA 120  
Db 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGQROHRARA 120  
QY 121 DGSISALVAPPPRAASSAPASIGLPGSQHTSIHPRSSNGSPPTVHISQSMNAASSGTSR 180  
Db 121 DGSISALVAPPPRAASSAPASIGLPGSQHTSIHPRSSNGSPPTVHISQSMNAASSGTSR 180  
QY 181 RSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQGEPAQORQKHRD 240  
Db 181 RSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQGEPAQORQKHRD 240  
QY 241 RDVPAQQRPAVHPAGPGPADRVGDPGRHRRARGOHQPRDGSQASRTVSGVPVSNV 300  
Db 241 RDVPAQQRPAVHPAGPGPADRVGDPGRHRRARGOHQPRDGSQASRTVSGVPVSNV 300  
QY 301 LSAGIRCRPTTTRAVAICLAATLASRGVVAQPGDVAAAAAGSPWPVRSVARPVAVLRT 360  
Db 301 LSAGIRCRPTTTRAVAICLAATLASRGVVAQPGDVAAAAAGSPWPVRSVARPVAVLRT 360  
QY 361 GPPRRPDSITQVGRPAVLFAPEQRCRRRADORSCRQIHPPGGRHVQIVASARGTVE 420  
Db 361 GPPRRPDSITQVGRPAVLFAPEQRCRRRADORSCRQIHPPGGRHVQIVASARGTVE 420  
QY 421 IGS 423  
Db 421 IGS 423

RESULT 10  
US-10-100-679-80  
; Sequence 80, Application US/10100679  
; Publication No. US20030054013A1  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; FILE REFERENCE: 11000.1042c2  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121  
; PRIOR FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: 09/450,072

```
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-100-679-80

Query Match          74.9%; Score 2145; DB 14; Length 582;
Best Local Similarity 67.4%; Pred. No. 1.3e-145;
Matches 442; Conservative 0; Mismatches 0; Indels 214; Gaps 4;

1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 93
61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRRRDVVGAGDAAAAGVGLGPQRHARA 120
94 HRSVGEVRGLGVFWA----- 108
121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
109 -GSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 167
181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQQRQKHRD 240
168 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGA----- 207
241 RRDVPAQORPAVHPAGPADRVGVDPGRHRRARGQHOPRQDSDRQASRTVSGVPVESNV 300
208 -----GSDRQASRTVSGVPVESNV 226
301 LSAGIRCRTPPTTRAIVAICLATLASRGVVAPQAGDVAAAAAGSPWVRSVARPVAVLRT 360
227 LSAGIRCRTPPTTRAIVAICLATLASRGVVAPQAGDVAAAAAGSPWVRSVARPVAVLRT 286
361 GPPRRPSDT----- 370
287 GPPRRPSDTGSDQLGEPGAQQRQKHRDRRDVPAQORPAVHPAGPADRVGVDPGRH 346
371 -----GSIITQVGRPAVLFAPEQRCRRRADQSCROIHPGCGGRHVQIVASARGTV 419
347 RRARGQHOPRQDGSITQVGRPAVLFAPEQRCRRRADQSCROIHPGCGGRHVQIVASARGTV 406
420 EIGSTARLCGKDEAVALHYVAPVGEKQYIDRALRNTGPYLPAAVPAV----- 469
407 EIGSTARLCGKDEAVALHYVAPVGEKQYIDRALRNTGPYLPAAVPAVVGSDPERAGLR 466
470 -----GSIATATGPVPGTAWIVRQYPKLLR 493
467 VEVLGAQCRRRDVVGAGDAAAAGVGLGPQRHARADGSIATATGPVPGTAWIVRQYPKLLR 526
494 AKANWEDTWTTPSIIEKHPRGSAVGPVFRVNLGRAIPSRARAARAEIHGSHHHHHH 549
527 AKANWEDTWTTPSIIEKHPRGSAVGPVFRVNLGRAIPSRARAARAEIHGSHHHHHH 582

RESULT 11
US-10-607-752-80
; Sequence 80, Application US/10607752
; Publication No. US2004007224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c3
; CURRENT APPLICATION NUMBER: US/10/607,752
; CURRENT FILING DATE: 2003-06-26
```

```
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-607-752-80

Query Match          74.9%; Score 2145; DB 15; Length 582;
Best Local Similarity 67.4%; Pred. No. 1.3e-145;
Matches 442; Conservative 0; Mismatches 0; Indels 214; Gaps 4;

1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 93
61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRRRDVVGAGDAAAAGVGLGPQRHARA 120
94 HRSVGEVRGLGVFWA----- 108
121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
109 -GSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 167
181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQQRQKHRD 240
168 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGA----- 207
241 RRDVPAQORPAVHPAGPADRVGVDPGRHRRARGQHOPRQDSDRQASRTVSGVPVESNV 300
208 -----GSDRQASRTVSGVPVESNV 226
301 LSAGIRCRTPPTTRAIVAICLATLASRGVVAPQAGDVAAAAAGSPWVRSVARPVAVLRT 360
227 LSAGIRCRTPPTTRAIVAICLATLASRGVVAPQAGDVAAAAAGSPWVRSVARPVAVLRT 286
361 GPPRRPSDT----- 370
287 GPPRRPSDTGSDQLGEPGAQQRQKHRDRRDVPAQORPAVHPAGPADRVGVDPGRH 346
371 -----GSIITQVGRPAVLFAPEQRCRRRADQSCROIHPGCGGRHVQIVASARGTV 419
347 RRARGQHOPRQDGSITQVGRPAVLFAPEQRCRRRADQSCROIHPGCGGRHVQIVASARGTV 406
420 EIGSTARLCGKDEAVALHYVAPVGEKQYIDRALRNTGPYLPAAVPAV----- 469
407 EIGSTARLCGKDEAVALHYVAPVGEKQYIDRALRNTGPYLPAAVPAVVGSDPERAGLR 466
470 -----GSIATATGPVPGTAWIVRQYPKLLR 493
467 VEVLGAQCRRRDVVGAGDAAAAGVGLGPQRHARADGSIATATGPVPGTAWIVRQYPKLLR 526
494 AKANWEDTWTTPSIIEKHPRGSAVGPVFRVNLGRAIPSRARAARAEIHGSHHHHHH 549
527 AKANWEDTWTTPSIIEKHPRGSAVGPVFRVNLGRAIPSRARAARAEIHGSHHHHHH 582

RESULT 12
US-10-100-679-94
; Sequence 94, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; TITLE OF INVENTION: and Methods for Their Use
```

```
FILE REFERENCE: 11000.1042c2
; CURRENT APPLICATION NUMBER: US/10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-100-679-94

Query Match      67.1%; Score 1919; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60
|||||
1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60

61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRDRDVVGAGDAAAAGVVGPGQRHARA 120
|||||
61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRDRDVVGAGDAAAAGVVGPGQRHARA 120

121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPTVHIQSMMNAASSGTSR 180
|||||
121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPTVHIQSMMNAASSGTSR 180

181 RSTLFRWQSPCMIPGSSAGLRESSQSASTCTDGNDSGAGSDQIGEFGAQQRQKHRD 240
|||||
181 RSTLFRWQSPCMIPGSSAGLRESSQSASTCTDGNDSGAGSDQIGEFGAQQRQKHRD 240

241 RRDVPAQQRPAVHPAGPADRVGVDPGHRRARQHQPRDGSDRQAASRTVSGVPVSNV 300
|||||
241 RRDVPAQQRPAVHPAGPADRVGVDPGHRRARQHQPRDGSDRQAASRTVSGVPVSNV 300

301 LSAGIRCTPTTTRAVAICLATLASRGVWAPQAGDVARAAAAGSPWPVRSVARPVAVLRT 360
|||||
301 LSAGIRCTPTTTRAVAICLATLASRGVWAPQAGDVARAAAAGSPWPVRSVARPVAVLRT 360

361 GPPRRPSDTGS 372
|||||
361 GPPRRPSDTGS 372

RESULT 13
US-10-607-752-94
; Sequence 94, Application US/10607752
; Publication No. US20040072224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c3
; CURRENT APPLICATION NUMBER: US/10/607,752
; PRIOR FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
```

```
US-10-607-752-94

Query Match      67.1%; Score 1919; DB 15; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60
|||||
1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60

61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRDRDVVGAGDAAAAGVVGPGQRHARA 120
|||||
61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRDRDVVGAGDAAAAGVVGPGQRHARA 120

121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPTVHIQSMMNAASSGTSR 180
|||||
121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPTVHIQSMMNAASSGTSR 180

181 RSTLFRWQSPCMIPGSSAGLRESSQSASTCTDGNDSGAGSDQIGEFGAQQRQKHRD 240
|||||
181 RSTLFRWQSPCMIPGSSAGLRESSQSASTCTDGNDSGAGSDQIGEFGAQQRQKHRD 240

241 RRDVPAQQRPAVHPAGPADRVGVDPGHRRARQHQPRDGSDRQAASRTVSGVPVSNV 300
|||||
241 RRDVPAQQRPAVHPAGPADRVGVDPGHRRARQHQPRDGSDRQAASRTVSGVPVSNV 300

301 LSAGIRCTPTTTRAVAICLATLASRGVWAPQAGDVARAAAAGSPWPVRSVARPVAVLRT 360
|||||
301 LSAGIRCTPTTTRAVAICLATLASRGVWAPQAGDVARAAAAGSPWPVRSVARPVAVLRT 360

361 GPPRRPSDTGS 372
|||||
361 GPPRRPSDTGS 372

RESULT 14
US-10-100-679-79
; Sequence 79, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c2
; CURRENT APPLICATION NUMBER: US/10/100,679
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-100-679-79

Query Match      66.6%; Score 1906; DB 14; Length 582;
Best Local Similarity 57.1%; Pred. No. 2e-128;
Matches 399; Conservative 0; Mismatches 0; Indels 300; Gaps 2;

1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60
|||||
34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 93

61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRDRDVVGAGDAAAAGVVGPGQRHARA 120
|||||
94 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRDRDVVGAGDAAAAGVVGPGQRHARA 153
```

```
Qy 121 ----- 120
Db 154 DGSQASRTVSGVPVSNVLSAGIRCTPTTTRAVAICLATLASRGVVAPQAGDVARAA 213
Qy 121 ----- 120
Db 214 AAGSPWVRSVARPVAVLRTGPPRRPSDTGSDQGEPAQQRQKRRDRDVPAAQORP 273
Qy 121 -----DGSISSALVASPPRAASAPASIGLPGSGQ 150
Db 274 AVHPAGPGPADRVGDPGRHRRARGQHPRDGSISSALVASPPRAASAPASIGLPGSGQ 333
Qy 151 HTSIHPRSSNGSPVTHISQSNMAASGTSRSSSTLFRWQSPCMIPGSASSGLRESSQSAS 210
Db 334 HTSIHPRSSNGSPVTHISQSNMAASGTSRSSSTLFRWQSPCMIPGSASSGLRESSQSAS 393
211 TCTDNDGSGAGSDQLGEPGAQQRQKRRDRDVPAAQORPAVHPAGPGPADRVGVDPCR 270
394 TCTDNDGSGA----- 403
Qy 271 RRARGQHPRDGSQASRTVSGVPVSNVLSAGIRCTPTTTRAVAICLATLASRGVVAP 330
Db 404 ----- 403
Qy 331 QPAGDVARAAAGSPWVRSVARPVAVLRTGPPRRPSDTGSIQVGRPAVLFAPEQR 390
Db 404 -----GSITQVGRPAVLFAPEQR 423
Qy 391 RRADQSCROIHPGGGRHVQIVASARGTVEIGSTARLCGKDEAAALHYVAPVGEKQDYI 450
Db 424 RRADQSCROIHPGGGRHVQIVASARGTVEIGSTARLCGKDEAAALHYVAPVGEKQDYI 483
Qy 451 DRALRNIGPYLPAEVPALVGSIAATGVPGTAWIVRQYPKLLRAKANWEDTWTTPPSIEEK 510
Db 484 DRALRNIGPYLPAEVPALVGSIAATGVPGTAWIVRQYPKLLRAKANWEDTWTTPPSIEEK 543
Qy 511 HRPRGSVAGPVFRVNLGRAIPSRARAABEIHGSHHHHH 549
Db 544 HRPRGSVAGPVFRVNLGRAIPSRARAABEIHGSHHHHH 582

RESULT 15
US-10-607-752-79
Sequence 79, Application US/10607752
Publication No. US2004007224A1
GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c3
; CURRENT APPLICATION NUMBER: US/10/607,752
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 582
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-607-752-79
```

Query Match 66.6%; Score 1906; DB 15; Length 582;  
Best Local Similarity 57.1%; Pred. No. 2e-128;  
Matches 399; Conservative 0; Mismatches 0; Indels 300; Gaps 2;

```
Qy 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIQEQVILGPGGLDLAAR 60
Db 34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIQEQVILGPGGLDLAAR 93
Qy 61 HRSYGEVRGLGVFWAGSDPERAGLRVEVLGAQCRRRDVWGAGDAAAAGVVLGPQQRHARA 120
Db 94 HRSYGEVRGLGVFWAGSDPERAGLRVEVLGAQCRRRDVWGAGDAAAAGVVLGPQQRHARA 153
Qy 121 ----- 120
Db 154 DGSQASRTVSGVPVSNVLSAGIRCTPTTTRAVAICLATLASRGVVAPQAGDVARAA 213
Qy 121 ----- 120
Db 214 AAGSPWVRSVARPVAVLRTGPPRRPSDTGSDQGEPAQQRQKRRDRDVPAAQORP 273
Qy 121 -----DGSISSALVASPPRAASAPASIGLPGSGQ 150
Db 274 AVHPAGPGPADRVGDPGRHRRARGQHPRDGSISSALVASPPRAASAPASIGLPGSGQ 333
Qy 151 HTSIHPRSSNGSPVTHISQSNMAASGTSRSSSTLFRWQSPCMIPGSASSGLRESSQSAS 210
Db 334 HTSIHPRSSNGSPVTHISQSNMAASGTSRSSSTLFRWQSPCMIPGSASSGLRESSQSAS 393
Qy 211 TCTDNDGSGAGSDQLGEPGAQQRQKRRDRDVPAAQORPAVHPAGPGPADRVGVDPCR 270
Db 394 TCTDNDGSGA----- 403
Qy 271 RRARGQHPRDGSQASRTVSGVPVSNVLSAGIRCTPTTTRAVAICLATLASRGVVAP 330
Db 404 ----- 403
Qy 331 QPAGDVARAAAGSPWVRSVARPVAVLRTGPPRRPSDTGSIQVGRPAVLFAPEQR 390
Db 404 -----GSITQVGRPAVLFAPEQR 423
Qy 391 RRADQSCROIHPGGGRHVQIVASARGTVEIGSTARLCGKDEAAALHYVAPVGEKQDYI 450
Db 424 RRADQSCROIHPGGGRHVQIVASARGTVEIGSTARLCGKDEAAALHYVAPVGEKQDYI 483
Qy 451 DRALRNIGPYLPAEVPALVGSIAATGVPGTAWIVRQYPKLLRAKANWEDTWTTPPSIEEK 510
Db 484 DRALRNIGPYLPAEVPALVGSIAATGVPGTAWIVRQYPKLLRAKANWEDTWTTPPSIEEK 543
Qy 511 HRPRGSVAGPVFRVNLGRAIPSRARAABEIHGSHHHHH 549
Db 544 HRPRGSVAGPVFRVNLGRAIPSRARAABEIHGSHHHHH 582
```

Search completed: September 16, 2005, 20:48:59  
Job time : 173 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2005, 20:44:49 ; Search time 43 Seconds  
(without alignments)  
1228.442 Million cell updates/sec

Title: US-10-607-752-116

Perfect score: 2862

Sequence: 1 IYSTFADRAYPGGLTSGHP.....IPSRARAARAEIHGSHHHH 549

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	273	9.5	451	2	T35390
2	182	6.4	1442	2	T42607
3	172	6.0	1446	1	A45344
4	169	5.9	775	1	EDBE11
5	166	5.8	686	2	A38235
6	166	5.8	1733	1	B45344
7	163.5	5.7	2274	2	T30258
8	157.5	5.5	1106	2	J00405
9	156.5	5.5	1958	2	B40505
10	156	5.5	2796	2	JC4743
11	151	5.3	660	1	Q0BE3
12	150	5.2	1952	2	T48814
13	148.5	5.2	744	2	T35192
14	147.5	5.2	426	2	B83611
15	147	5.1	1298	1	EDBE75
16	147	5.1	13288	2	T03099
17	145.5	5.1	1334	2	T50568
18	144	5.0	1217	2	T00270
19	144	5.0	1329	2	T29074
20	142	5.0	1616	2	T17884
21	141.5	4.9	733	2	A45301
22	141.5	4.9	2082	2	T37056
23	140.5	4.9	924	2	S27923
24	140	4.9	825	1	EDBE3D
25	139.5	4.9	427	2	AF0839
26	139.5	4.9	1460	1	EDBE1F
27	139	4.9	1122	2	T14180
28	138	4.8	1487	1	EDBE1
29	137.5	4.8	862	2	T46289

30 137.5 4.8 1496 1 CGHU2V  
31 136.5 4.8 676 1 EDBE23  
32 136.5 4.8 1487 1 EDBE76  
33 136 4.8 467 2 T25848  
34 136 4.8 1607 2 T02837  
35 135.5 4.7 538 2 S57459  
36 135.5 4.7 888 2 S28791  
37 134.5 4.7 2240 2 T37057  
38 134 4.7 1791 2 T02345  
39 133 4.6 1093 2 T38533  
40 133 4.6 1678 2 T35547  
41 132.5 4.6 444 2 G90446  
42 132.5 4.6 3869 2 A48205  
43 132 4.6 527 2 A75399  
44 132 4.6 2142 2 B35098  
45 131 4.6 317 2 S55316

#### ALIGNMENTS

##### RESULT 1

T35390

probable aminotransferase - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004

C/Accession: T35390

R/Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1999

A/Reference number: Z21576

A/Accession: T35390

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-451 <MUR>

A/Cross-references: UNIPROT:Q9XAI0; EMBL:AL079348; PIDN:CAB45489.1; GSPDB:GN00070; SCOE

A/Experimental source: strain A3(2)

C/Genetics:

A/Gene: SCOE:DB:SC66T3.33

C/Superfamily: ornithine-oxo-acid aminotransferase

Query Match 9.5%; Score 273; DB 2; Length 451;

Best Local Similarity 69.3%; Pred. No. 1.8e-09;

Matches 52; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 IYSTFADRAYPGGLTSGHPLATACAVATINAMEDEGMVANAARIGQVLPGLRDLAAR 60

Db 298 IAATFAERPYPGGLTSGHPLACAAAVATINVMACGVVEHAARLGAEVVEPALRELAER 357

Qy 61 HRSVGEVRGIGVFWA 75

Db 358 HPSVGEVRGIGVFWA 372

##### RESULT 2

T42607

transcription activator - equine herpesvirus 4 (strain NS80567)

C/Species: equine herpesvirus 4

A/Variety: strain NS80567

C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C/Accession: T42607; T42622

R/Telford, E.A.; Watson, M.S.; Perry, J.; Cullinan, A.A.; Davison, A.J.

J. Gen. Virol. 79, 1197-1203, 1998

A/Title: The DNA sequence of equine herpesvirus-4.

A/Reference number: Z22173; MUID:98264497; PMID:9603335

A/Accession: T42607

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1442 <TEL>

A/Cross-references: UNIPROT:O42066; EMBL:AF030027; NID:G2605950; PIDN:AAC59599.1; PID:G2

A/Experimental source: strain NS80567

A/Accession: T42622

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A;Residues: 1-1442 <TE2>  
A;Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AA059599.1; PID:g2606027  
A;Experimental source: strain NS80567  
C;Genetics:  
A;Gene: 64  
C;Superfamily: herpesvirus immediate-early protein IE175

Query Match 6.4%; Score 182; DB 2; Length 1442;  
Best Local Similarity 21.4%; Pred. No. 0.0021;  
Matches 136; Conservative 47; Mismatches 170; Indels 282; Gaps 28;

QY 5 PADRAYP-----GGLTSGHPLATACAVATINAMEDEGMVNAARIGEQ----- 48  
DB 542 YADWAYPRDDAGRODSHSAAGVTASYPAQAQ-----ASQPDPPATSAKREEYTRV 594  
QY 49 -----VLGPGFLR---DLAARHSVGEV-----RGLGVFWAGSDP 79  
595 CAALGPRRKTAAGGPTRTPKPTAFRLRLRELDGVCVLACQAVFEALLRLRGASAVPGCLDP 654  
80 ER-----AGLREVLGAQC---RRDVVG-----AGDAAVCVLGPORQH- 116  
DB 655 SEIPSPACPPALCSNPAGLET-----AACALYELDLIVERARLLGDSDPHRLGPDDELRL 710  
QY 117 -----PARADG-SISSALVASPPRAASSAPASIGLGPSSQHT 152  
DB 711 AVRAVLVVARTVAPLVRYNAEGARARASAWTITQAVFSIFSLAGMLGEAVGL----- 763  
QY 153 SIHPRSSNGSPV--HISQSMNAASGTSRRSSTLFRWQS---PCMIPGS---ASSGL 202  
DB 764 -LAPPRSQSSSVGDDVGGQQSLSSSEGSQTSRIPALWPTVPGKPLVVPATSHSQSSPQ 822  
QY 203 RESQSASTCTDNDSCA---GSQDLPGEPAQO----- 232  
DB 823 HQSSGGPTTSRATQTQAPRSGQKARSPAPASQAILQOEMPVSSQGGGPPAPYASPNDRP 882  
QY 233 --RQGRKRRDRDVPAAQRPVHPAGPGPADRVGDPGRHRRAGQHQPRDGSDDQASR 289  
DB 883 VNGRPRKSKKRREPLE--PA---AGELPGSGYGVDFVAPSPVPAPKRVGT--QAPR 935  
QY 290 TVSGVPVSVNLASGIR-----CRTPTRAVAICLATLASRGVAPQAGDVARAAAAG 343  
DB 936 ALGMPMPGEGHRRGGFRVPHGDCHTP-----PPGDSARAAYC- 973  
QY 344 SPWPVRSVAPVAVLRITGPPRRPSDTGSIQVGRPAVLPAPEQRRCRRADQSCRQIHP 403  
DB 974 ---PPELVAELI-----DHPLPPEAWRPALTDPDQ----- 1000  
QY 404 GGRHRVQIVASAGTVEIGSIARLCGKDEAAALHYVAVGEXQDYIDRALRNIGPYLPA 463  
DB 1001 -----ALATIAARN-----GP--PA 1014  
QY 464 EVPALVGSIAATGPVPGTAWIVROYPKLLRAKANW 498  
DB 1015 REGARFGELAASGP-----LRRRAAW 1035

RESULT 3  
A45344  
immediate-early protein - suid herpesvirus 1 (strain Kaplan)  
C;Species: suid herpesvirus 1  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: A45344  
R;Vicek, C.; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzler, M.  
Virology 179, 365-377, 1990  
A;Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented or  
A;Reference number: A45344; MUID:91021039; PMID:2171211  
A;Accession: A45344  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1446 <VLC>  
A;Cross-references: UNIPROT:P33479; GB:M34651; NID:g334070; PIDN:AAA47470.1; PID:g334071  
C;Superfamily: herpesvirus immediate-early protein IE175  
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 6.0%; Score 172; DB 1; Length 1446;  
Best Local Similarity 21.3%; Pred. No. 0.0085;  
Matches 154; Conservative 54; Mismatches 224; Indels 290; Gaps 31;

QY 27 VATINAMEDEGMVNAARIGEQVLPGLRDLAARHR-SVGEVRLGLGVFWAGSDPERAGLR 85  
DB 19 LAAAAAEEEGTAS-----GPDGSGQSRRRSGSGEDLLFGPGLFSD--DAEAE 67  
QY 86 VEVLGAQCRRRDVGAGDAAVGVLP-----ORQHRARADGSI-----S 125  
DB 68 AAVL-----AAAAGATPPPPSAQQQQQPRGSGEIVLDDDEDEDEPG 113  
QY 126 SALVASPPRAASAPASIGLSPSGOHTSIHPRSSNGS---PTVHISQSMNAASGTSRR 181  
DB 114 SPAAGSPGGA-----LHQSSEHGHVLGPRSRAGSGPRPTPAALAAAEAGAPGPGQR 166  
QY 182 SSTLFRWQSPCMTPGSASSGLRESSQSASTCTDNDGSGAGSDOLGEPGAQQQRQGRHRR 241  
DB 167 SSP-----SAASPASSSGSPGSAAPRRWSPARGDPVGEPPAARPTPAPPA 214  
QY 242 RD-----VPAQORPAPVHPAGP-----GPADRVGVDPGRH-----R 271  
DB 215 QPAAVAAAARRGPA--SPASPAAGPVSAFGGGAAGSAGGDRGHHHQRHREPLLDPAAR 273  
QY 272 R-----ARG-----QHQR-- 280  
DB 274 RLDPRLGARSFVSSNNPNSNSTTTTAVETVARQPEKDEGLGLAGDGGAPPQRPQRRR 333  
QY 281 -----DGSD-----RQASRTVSGVPVSVNLVS 302  
DB 334 RAGEALRRGRGFSSSSSGSDLSPARSPAPRAAAAAARRRASSSSSSSSSSSSSS 393  
QY 303 A-----GIRCTPTTTRAVAICLATLASRG-----VVAPQAGDVARAAAAGSP 345  
DB 394 SSSSEGEDEGVPCGAPLARA-----GPPPSPPAPAAAPRPSASSASSAAASP 442  
QY 346 WPVRSVARP-----VAVLTGTPPPRPSDTGSIQVGRPAVLPAPEQRRCRRRA- 393  
DB 443 APAPEAPRPRRKRRTNNHLSLMADGPP---PTDGPLLTPLGEPWPGSDPPADGVRVYG 499  
QY 394 -----DQSCRQIHPGGGRHVQIVASARGTV-----BIGSIARLCGKDEAAALH 438  
DB 500 GAGDSREGLWEDDDVQO---AAARY-----RAAGVPVPIPEMGDSRK---QHEALVRLI 549  
QY 439 YVAPVGEKQDYD-----RALRNIQGYLPAPV-----PALVGSIAAT 475  
DB 550 YSAGAGEAMSWLQNPQPMQAPDQRFNQFCQRRVHAPHGHGSFITGSVTPPLPHIGDAMAAQ 609  
QY 476 GPVPGTAWIVROYPKLLRAKANWEDTWTTPSIEEKHPRGSGVAGPVFRVNLGRAIPSRAA 535  
DB 610 DPL-----WALPHAVSAVAMSRRYDRTQKTFILQSLRRAYADWAYP-----GRAADPRAG 659  
QY 536 RA 537  
DB 660 EA 661

RESULT 4  
EDBE11  
immediate-early protein IE110 - human herpesvirus 1 (strain 17)  
C;Species: human herpesvirus 1  
C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
C;Accession: A29152  
R;Perry, I.J.; Rixon, F.J.; Everett, R.D.; Frame, M.C.; McGeoch, D.J.  
J. Gen. Virol. 67, 2365-2380, 1986  
A;Title: Characterization of the IE110 gene of herpes simplex virus type 1.  
A;Reference number: A29152; MUID:87059760; PMID:3023529  
A;Accession: A29152  
A;Molecule type: DNA  
A;Residues: 1-775 <P>  
A;Cross-references: UNIPROT:P08393; GB:X04614; NID:g59832; PIDN:CAA28285.1; PID:g59833  
C;Genetics:

A: Introns: 19/3; 242/1  
C: Superfamily: herpesvirus immediate-early protein IE110; RING finger homology  
K: Keywords: DNA binding; early protein; transcription regulation; zinc finger  
F: 112-162/Domain: RING finger homology <RNG>  
F: 116-156/Region: zinc finger C3HC4 motif

Query Match 5.9%; Score 169; DB 1; Length 775;  
Best Local Similarity 23.4%; Pred. No. 0.0066;  
Matches 118; Conservative 38; Mismatches 164; Indels 184; Gaps 27;

QY 111 GPQQRARADGSISSALVASPPRAASAPASIGLG-----PSGQHTSI-----HP 156  
DB 307 GGSQSRAAA-----PRGASGSGGVGVGVVPAEAGRPGRGTGPIVNRPA 354  
QY 157 RSSNGSPVTHISQS-----MNAASSTGSRSSSTLFRWQSPCM 193  
DB 355 LANNEDPIV-LSDPASPSPHPRAAPMGSAAPRGPPASAAAGPAPRAAV-----APCV 409  
QY 194 -----IPGSASSGLRESSQSASTCTDGNDSGAGSDQLG 226  
DB 410 RAPPPGPRAPAPCAEPAAPADARRVPQSHSSLAQAANQESILCRARATVARGSG 466  
QY 227 EPQAQORQGRHRRDRVPAQORPAVHPAGPGPADRVGDCGRHRRARGQHPRGDSRQ 286  
DB 467 GPGVE-----CGHGPSRGA-APSGAAPLPSAASVEQEAARVP-RKRRSGQENPSPQSTRP 520  
QY 287 -----ASRTVSGVPVESNLSAGIRCR-----TPTRAVAICLATLASRGVVAQPADGV 336  
DB 521 PLAPAGAKRANTHPPDS-----GPGRGGGGTGPTLTSSAASASSSSASS-SATTPAGAA 576  
QY 337 ARAAAGSPFWRVSRVAVVL-----RTGPPRRPSPDTGSIITQVGRPAVLFP 385  
DB 577 SSAAGAASSASASSGAGVALGGRQETSLGPRASGPRGP----- 618  
QY 386 EQRERRADQSCRQIHPPGGHVOIVASAGTVEIGSIAR-----LCKDKEAVALHYV-- 440  
DB 619 -RKCARKT-----RH-----AETSGAVPAGGLTYLPISGVSSVVALSPYVVK 660  
QY 441 APVEKQDYIDRALRNIGPYLPAEVPALV-----GSIAA--TGPVPGTAVIR----- 486  
DB 661 TITGDCPLDMETGNIGAYV-----VLVDQTGNMTRLAARVPG--WSRRTLLPETAGN 713  
QY 487 -----QYPKLLRAKANWEDTTFP 505  
DB 714 HVMPPEYF--TAPASEWNSLWMP 735

RESULT 5  
A38235  
A: Title: microtubule-associated protein, 110K tau - rat  
C: Species: Rattus norvegicus (Norway rat)  
C: Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C: Accession: A38235  
R: Goedert, M.; Spillantini, M.G.; Crowther, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 1983-1987, 1992  
A: Title: Cloning of a big tau microtubule-associated protein characteristic of the perip  
A: Reference number: A38235; MUID: 92179305; PMID: 1542696  
A: Accession: A38235  
A: Molecule type: mRNA  
A: Residues: 1-686 <GOE>  
A: Cross-references: UNIPROT: P19332; GB: M84156; NID: g207157; PIDN: AAA42204.1; PID: g207158  
A: Note: sequence extracted from NCBI backbone (NCBI: 87358, NCBI: 87359)  
C: Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology  
C: Keywords: alternative splicing; microtubule binding; tandem repeat  
F: 497-527/Domain: MAP2/tau repeat homology <MT1>  
F: 528-558/Domain: MAP2/tau repeat homology <MT2>  
F: 559-589/Domain: MAP2/tau repeat homology <MT3>  
F: 590-621/Domain: MAP2/tau repeat homology <MT4>

Query Match 5.8%; Score 166; DB 2; Length 686;  
Best Local Similarity 22.8%; Pred. No. 0.0088;  
Matches 132; Conservative 69; Mismatches 189; Indels 188; Gaps 33;

QY 36 EGMVANAARICEQVLGFLRLDLAARH-----RSVGEVRLGVF-W 74  
DB 88 EGTITABEAGIDT---PNMEDQAAGHTVQBPQKVEIFSQILLSLVEPGRREGQAPDSGISDW 144  
QY 75 -----AGSDPERAGLRV---EVLGAQCRRRDVVAGDAA-AVGVLGPOR----- 114  
DB 145 THQQVPSMSGAPLPPOGLREATHQPLGT--RPEDVERSHPASELLWQESQKEAWKDRL 202  
QY 115 --QHRARADGSISSALVASPPRAASSAPASI-----GLGPSGQHTSIHPRSSNGS-- 162  
DB 203 GSEBEVDITDMESSOESPQSALAPGTATPAQARSVSASGSGSETTISIPGFPAGSIP 262  
QY 163 -PTVHISQSMNAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGA- 220  
DB 263 LPADFFSK---VSAETQ-----ASPEPGTGTGS--EEGHEAAPETTFHVEIKAS 307  
QY 221 -----GSDQGEPAQQRQKQH--RDRRDV---PAQORPAVHPAG-PG-PADRVG 264  
DB 308 APKEQDLEGATVVGAPAEQKARGPSVGKGTKEASLLEPTDKQPA---AGLPGRPVSRV- 363  
QY 265 VDCGRHRRARGQHPRGDSRQASRTVSGVPVESNLSAGIRCRTP-----TTTRA 314  
DB 364 --POLKARVAGVKDRGTGNDKKAAGADG-----KTGAKIATPRGAATPGQKGTGNA 413  
QY 315 VAICLATLAS-----RGVVAPOQPADVARAAAAGS-----PWPVRSVARPVAV 357  
DB 414 TRIPAKTTPSKTPPGSGEBPPKSGERSGYSSPGSGPTGSRSTPSTLPTTPREPKKAV 473  
QY 358 LRTGPPRRPSDTGSIITQVGRPAVLPAPE-ORCRRRADQSCRQIHPPGGHVOIVASAR 416  
DB 474 VRT--PPKSPSASKSLQT---APVMPDLKNVRSKIGSTENLKHQPGGK-VQII--N 524  
QY 417 GTVEIGSIARLCKDKEAV-----AALHYV-APV----- 443  
DB 525 KLDLSNVQSKGSKONIKHVPGGSGVHIYKPVLSKVTSGKSLGNIHHKPGGQVEV 584  
QY 444 -GEKQDYIDRALRNIGPYLPAEVPALVGSIAATGPPVPG 480  
DB 585 KSEKLDFKDR-----VQSKIGSLDNITHVPG 610

RESULT 6  
B45344  
A: Title: probable nuclear antigen - suid herpesvirus 1 (strain Kaplan)  
C: Species: suid herpesvirus 1  
C: Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C: Accession: B45344  
R: Vlicek, C.; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzer, M.  
Virology 179, 365-377, 1990  
A: Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented op  
A: Reference number: A45344; MUID: 91021039; PMID: 2171211  
A: Accession: B45344  
A: Status: translation not shown  
A: Molecule type: DNA  
A: Residues: 1-1733 <UNIC>  
A: Cross-references: UNIPROT: P33485; GB: M34651; NID: g334070; PIDN: AAA47471.1; PID: g334072  
C: Superfamily: pseudorabies virus 1 nuclear antigen

Query Match 5.8%; Score 166; DB 1; Length 1733;  
Best Local Similarity 23.2%; Pred. No. 0.024;  
Matches 142; Conservative 45; Mismatches 218; Indels 208; Gaps 29;

QY 13 GLTYSGHPLATAC--AVATINAMEDGQV---ANAAIRIGQVL----- 50  
DB 786 GVGVLPHPGGAAAEARGAARFQVQGRVGEGERAPFEGEDLLVHEGAGHLGRAVGEGR 845  
QY 51 --GPGLRLDLAARHSVGEVRLGVFWAGSDPERAGLRVVEVLGAQCRRRDVVAGDAAAVG 108  
DB 846 LGGPRRVGLAGRDAAEAHV-GRGVL--GHCPRAPPEV-VLGGG-----GGGQQRGSG 895  
QY 109 V-LGPQRQHRARADGS-----ISSALVASP-----PRAASSAPASIGLPGSG 149  
DB 896 VRSGPESGAALAPGPPVLFVAVAVAPAEGRAGEPLVLLAVPGAAGPRAALLAPLG 955



A; Cross-References: UNIPROT:Q69340; GB:M57505; NID:G334066; PIDN:AAA47468.1; PID:G334068  
C; Superfamily: pseudorabies virus 1 nuclear antigen

Query Match	5.5%	Score 156;	DB 2;	Length 2796;
Best Local Similarity	22.3%;	Pred. No. 0.16;		
Matches 148;	Conservative	59;	Mismatches 216;	Indels 242;
Gap#	34			
Qy	1	IYSTFADRAYPGGLTYS-GHPLATACAVATINAMEDGMVANAAARIGEQVLGPGRLDLAA	59	
Db	204	IVAGNAEKA---GLDVALARELADAILIRKVDWDEITRVHRAGARWILDGPG--DILT	258	
Qy	60	RHRSGVEVGLGVFWAGSDPERAGLRVEVLGAQCRRRDVAGDAAVGLVGPOQRHAR	119	
Db	259	R-LTAPVIRGLGI--GIVPAR-----TRGGQ--RNLFVTGATPEV-----AR	295	
Qy	120	ADGSISSALVASP-----PRAASSAPASI-GLGPGSQHTSIHPRSSNG-----	161	
Db	296	AWESYAPTVVLPDGRVKLSTKTRLTTRRSPILLAGMTPTVDAKIVAAAANGRHWAELA	355	
Qy	162	-----SP---TVHISQSNAAASGTSRRSSSTLFRWQSPCMIPGSASSGLRSESSQASACTD	214	
Db	356	ARGSRPKRSVTTASNKPWACSSRAAPISST--RCSS---IPTCEASGROAVGAEGPPVR	410	
Qy	215	GNDSGAGSDQLGPGGAQO-----RORSGK-----RDRDVP---AQRPVAVHPAGP	257	
Db	411	RRDRRG-DQRHPRPRGRADRRYGRHRHQPRRVQTRDHRADPLGDSHHRGCAHQAGD	469	
Qy	258	-----GPADRVGVDVGR-----HRRARGOHQ-----PRDG-----	282	
Db	470	HARRGPGACAGTTPGRI SHLLLATYSADRAPRQHVCVGGGHLGTPKKGCGYLSPGGRSV	529	
Qy	283	-----SDRQ-----ASRTYSGVPVYES-----NVLSAG-----IRCR	308	
Db	530	RLPIDADRIILVGTAAATKESTTSSEVKWMLVDQTQDWISAGKAQGRMPPAESARCR	589	
Qy	309	TPTTT---AVAIC-----LATLASRGVAPQAPAGDVAR-----AAAAGSPWPVRSV	351	
Db	590	HPDRHSASVRRCTRWPTVTRRSRSVAVPRPPSPTCRRRRHDLPAVAAGATSNWPSPGKA	649	
Qy	352	ARVAVLRTGPPRRPSDGTISIQVGEPAVLFAPEQECRRRAQORSCR-----	399	
Db	650	TRP-----PTPRWAARGWPTLAG-----PURADAAACRSPVAPTTGPRPDP	690	
Qy	400	-----QIHFGG-----GRHVQIVASARGTV	419	

Db 691 DAIRHCWPAGSAAAIALVALVARYDPAETVQLHPADVPFFVTLCKTKLPNVFPAIDLVV 750  
Qy 420 EIGSIARLCGKDEAVA-----ALHYVAPVGEKQYIDRALRNIQYLPFAEVPALVGSIAA 474  
Db 751 RAGCAATRCGRPTTPTATPMRCASFRAVRGSR---ITRMDPEVGCGLLDAFEQAIDVILG 807  
Qy 475 TGPVP 479  
Db 808 AGVEP 812

RESULT 11  
QOBE3  
BHLF1 protein - human herpesvirus 4 (strain B95-8)  
C:Species: human herpesvirus 4, Epstein-Barr virus  
C>Date: 25-Feb-1985 #sequence\_revision 25-Feb-1985 #text\_change 09-Jul-2004  
C:Accession: A03742  
Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.  
Biol. Med. 1, 21-45, 1983  
A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus  
A:Reference number: A93065; MUID:85035713; PMID:6092825  
A:Accession: A03742  
A:Molecule type: DNA  
A:Residues: 1-660 <BAN>  
A:Cross-references: UNIPROT:P03181  
R;Bankier, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H  
Nature 310, 207-211, 1984  
A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.  
A:Reference number: A03794; MUID:84270667; PMID:6087149  
A:Contents: annotation; protein coding region  
C:Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-52  
C:Superfamily: human herpesvirus 4 BHLF1 protein

Query Match 5.3%; Score 151; DB 1; Length 660;  
Best Local Similarity 27.4%; Pred. No. 0.069;  
Matches 131; Conservative 25; Mismatches 188; Indels 134; Gaps 27;

Qy 100 GAGDAAVGVLGQRQH-RARADGSISSALVAGPPRAASGAPASIGLPGSQHTSIHPRS 158  
Db 219 GPADPPAAARLPPERQEPRLPQDLAAQRCPCAGPPTTRSGAAA-----QRTTHRRP-- 268  
Qy 159 SNGSPVTHISQSMNAASGTSRRSTLFRWQSPCMIPG-----SASSGLRESSQSA--ST 211  
Db 269 -PGCF-----RSARNPCPTWRRRSGAQRGHP--PGAQRSRGPTGPPAAGPAGPTP 320  
Qy 212 CTGNDGSA-----GSDQLGEPGAQ--RQRGKRRDRDVPAAQRPFAVHPAGP 257  
Db 321 AAPGPGGAAVPSGATPHPERGSGPADPPAAARLPPERQEPRLPQDLAAQRCPCAGP 377  
Qy 258 GPADRVGV-----DPGHRRRARGQHPDRGSDRQASTVSGVPVSNVLSAGIRCT 309  
Db 378 -PPTRSGAAQRTTHRRPFGCPSARNPCPTWRRRSGAQRGHP--GAGQRP 430  
Qy 310 PTTTAVAIATLASRGVAPQAGDVARAAAAGSPWPR--SVARFVAVLRGTP--PP 364  
Db 431 PTGERPA--APGAGTTPAAGCGGAAVPSGA--TPHPERGSGPADPPAAARLPPERQEP 486  
Qy 365 RRPDSGTSITQ--VGRPAVL--APEQRCRRAD--QRSCQIHPGGRHVQIVASA-RGT 418  
Db 487 RLPQDLAAQRCPCAGPPTTRSGAAQRTTHRRPFGCPSAR--NFGCPTWRRRSGAQRGH 544  
Qy 419 VEIGSIARLCGKDEAVAALHYVAPVGEKQYIDRALRNIQYLPFAEVPALVGSIAATGPV 478  
Db 545 PPPGAGQRP--PTGGR-----PTGGR-----PA-APGAGPTTAAAPGPG 576  
Qy 479 PGTAWIVRQYKPLLRKANWEDTTFPSIEKHPRGSGVAGPVRNIGRAIPRAAR 536  
Db 577 GGAA-----VFSGATPHPERG-----GPADPPAAR 603

RESULT 12

T48814

hypothetical protein 1586.220 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C&gt;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004

C:Accession: T48814

R;Schulte, U.; Align, V.; Hobeisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
submitted to the Protein Sequence Database, April 2000

A:Reference number: 224541

A:Accession: T48814

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1952 &lt;SCH&gt;

A:Cross-references: UNIPROT:Q9P6T1; EMBL:AL353822; GSPDB:GN00112; NCSP:1586.220

A:Experimental source: cosmid contig 1586; strain 74

C:Genetics:

A:Gene: NCSP:1586.220

A:Map position: 2

A:Introns: 281/3

Query Match 5.2%; Score 150; DB 2; Length 1952;

Best Local Similarity 22.0%; Pred. No. 0.25;

Matches 135; Conservative 56; Mismatches 246; Indels 176; Gaps 27;

Qy 11 PGGLTYSGHPLATACAVATINAMEDGVMANARIGEQLVGLGRLDLAARHSVGEVRGL 70

Db 1292 PRAAPISGHPIAP-----STVNN-----TNAAM-----GARVPA----- 1321

Qy 71 GVFWAGSDPERAGLRVEVLGAQCRRRDVVAGDAAAVGLGPRQHRARADGSISSALVA 130

Db 1322 -----AVPGPQ-----IGVHSGAAGVTPAVRSRPPVTHGVVTAAPT 1359

Qy 131 SPRAASSAPASIGLPGSQHTSIHPRSNGSPVTHISQSMNAASGTSRRS-----STLF 186

Db 1360 TP---RSNLAAVFPAGSMAQQT---HSGAPAGSGNASISRAPPTAAPTTSVPPVSSTV 1414

Qy 187 RWQS--PCMIPGSASSGLRESSQASTCTGNDGSGAGSDQLGEPG-----AQQR 235

Db 1415 RPSYVTPGPGGLTAPPTASSGASAGYARPANASTPATISGQAAMTSVAVPOSVPSPRS 1474

Qy 236 GKHRDRDVA-----QQRPAVHPAGPGPADRVGDVDPGRHRRARGQHPRDGSDRQASRT 290

Db 1475 SLTTGQMGVPAIAAAASTSRPASGVNYP--PASSLA--PSTHK-----SMPSAVPT 1520

Qy 291 VSGVPVSNVLSAGI-----RCRTPTTAVAIATLASRGVAPQAGDVA 337

Db 1521 TASGAVSSTVSSLAATPLPSAPRYGPSNNATPTTATAPRAPLPAASSVAPVTGQPS 1580

Qy 338 RAAAGSPWPRVSA-----RPVAVLRTPPPRRPSDTSITQV-----GRPAVLFA 385

Db 1581 FSAPASVPTPTTSAASQGAQLSQPV-----GPAPAISSSIGATPAASTPSSAPALAPV 1635

Qy 386 EQRRCRRARQRCR-QIHFGGGRH--VQIVAS--ARGTVE--IGSIAR-LCGKDEAVAAL 437

Db 1636 TYPVPOQASAAAARLFTVPAPAAHTIAQSVAFVPTQSPVQSVQVACHVTSQASTTAA 1695

Qy 438 HVVA-----PVCEK-----QDYIDRALRNIQYLPFAEVPALVG 470

Db 1696 HPVAGSVPRVSNPTSAAPVAAVGAQTAVASAPVTQAPAPHRALSSVLSQSVPHAAQ 1755

Qy 471 SIAATGFVPGTAWIVRQYKPLLRKANWEDTTFPSIEKHPRGSGV-----GPVF 522

Db 1756 QAAHQTFHSASRPVQSVFPQ-----SVFQATQAVPRPSTSLTPTAQGPVS 1803

Qy 523 RVNLGRAIPRAA 535

Db 1804 PAVSGSGVPAPSA 1816

RESULT 13

T35192

probable ABC transporter - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C&gt;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004

C:Accession: T35192

R;Seeger, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, April 1998

A;Reference number: 221571  
A;Accession: T35192  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-744 <SE>  
A;Cross-references: UNIPROT:O69995; EMBL:AL02374; PIN:CAA18516.1; GSPDB:GN00070; SCORE  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Gene: SC05B8.08

Query Match 5.2%; Score 148.5; DB 2; Length 744;  
Best Local Similarity 24.2%; Pred. No. 0.11;  
Matches 130; Conservative 53; Mismatches 215; Indels 139; Gaps 27;

QY 18 GHPLATA-----CAVATTNAMEDEGMVANAARIGEOVLGPGRLDLAARHRSVGEVRL 70  
DB 85 GHFARTVRGHLRMLCAAGV-----PVRRADVEVLSVGLLGRDLRSLRSGMDRL 137  
QY 71 GVFWA-GSDP-----ERAGLRVEVLGAQCRRRDVGAGDAAVGVGLGPGQRHRRADGS 123  
DB 138 GLACALVPDPHTLVFDDPAG-----ALSAHDAR--GLHGALRAHAQAQGTIV 181  
QY 124 ISSALVASPPRASSAPASIGL-----GPSGQHTSIHPRSSNGSPVTHISQMN 173  
DB 182 LFS--TADPKAARSADHVVTLEGRVVDQEAAEFSRTLRPRVAVRSPPHAARLAALVT 239  
QY 174 ASGSTSRSTLRWQSPCMIPGSASSGLRESSQSASTCTDNDGAG-----SDQL 225  
DB 240 KEAARAARVSEVVR-----EGGNRLVYGSTCADIGEAFAFRHILVHQLADEV 287  
QY 226 GE--PGAQQRQGRKRRDRDVPQAQRPV-----HPAGPG---PADRVGVDPGRHRR 272  
DB 288 GDMGPGAGEIPAAQQRERREADGEPGTLSNAGRPGPTGVLLPSPATEGEPLDGR 347  
QY 273 ARGQHOPRDG-----SDRQASRTVGVVPVSNVLSAGIRCTPTTTRAVAILCAT 321  
DB 348 GAG-HGDDGDPASVAVPNRTFGPRQAPVAPVSGHGEA-----APSPAPAPGPSE 396  
QY 322 LASRGVVAPOPAGDVAARAA--AAGSPWPSVSVARVPVAVLTGPPRRPSDTGSIQVGRP 379  
DB 397 PAS-GPSAPAP-GPPAPAGPSAPAPGSPAPAGPSA---PAPGPSEPAGSPAPAG-P 450  
QY 380 AVLFAPEQRKRRADORSQRIIPGGGRHVQIVASARGTVEIGSIARLCGKDEAVAAALHY 439  
DB 451 SALDAEPLR-----TPFPFALVPGSARTREATATLPPISVRS-----APSPLEPLRY 499  
QY 440 V--APVGEKQDYIDRALRNTGYPVPAEPVPAVLSIAATGPVPGTAMIVROYPKLLRA 494  
DB 500 ELRRVAVGRTGFTGAV---VLLVSAVAVV--LARVGHTP-----QPRLLAA 542

RESULT 14  
B83611  
4-aminobutyrate aminotransferase PA0266 [imported] - Pseudomonas aeruginosa (strain PA01  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: B83611  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A;Reference number: B82950; MUID:2043737; PMID:10984043  
A;Accession: B83611  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-426 <STO>  
A;Cross-references: UNIPROT:Q916M4; GB:AE004465; GB:AE004091; NID:g9946107; PIDN:AG036  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: gbtT; PA0266  
C;Superfamily: ornithine-oxo-acid aminotransferase

Query Match 5.2%; Score 147.5; DB 2; Length 426;  
Best Local Similarity 33.7%; Pred. No. 0.07;  
Matches 34; Conservative 23; Mismatches 35; Indels 9; Gaps 3;

QY 7 DRAYPGGL--TVSGHPLATACAVATTNAMEDEGMVANAARIGEOVLGPGRLDLAARHRSV 64  
DB 288 DATAPOGLGTYAGSTIACAAALAVLKVFEELKSLRSQAVGBR-LKAGLREIQAKHKVI 346  
QY 65 GEVRGLG-----VFWAGSDPERAGLRVEVLGAQCRRRDVV 99  
DB 347 GDVRGLGSMVAIELFEGGDTHKPAABELVSKIVVRAREKGLI 387

RESULT 15

EDBE75  
immediate-early protein IE175 - human herpesvirus 1  
C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
C;Accession: A23510  
R;McGeoch, D.J.; Dolan, A.; Donald, S.; Brauer, D.H.K.  
Nucleic Acids Res. 14, 1727-1745, 1986  
A;Title: Complete DNA sequence of the short repeat region in the genome of herpes simple  
A;Reference number: A23510; MUID:86148504; PMID:3005980  
A;Accession: A23510  
A;Molecule type: DNA  
A;Residues: 1-1298 <MCG>  
A;Cross-references: UNIPROT:P08392; GB:X14112; GB:D00317; GB:D00374; GB:S40593; NID:g194  
C;Comment: This protein acts at the transcriptional regulatory level and is required thr  
C;Genetics:  
A;Gene: IE3  
A;Map position: short repeat region (IR-s)  
C;Superfamily: herpesvirus immediate-early protein IE175  
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 5.1%; Score 147; DB 1; Length 1298;  
Best Local Similarity 22.2%; Pred. No. 0.25;  
Matches 136; Conservative 56; Mismatches 205; Indels 216; Gaps 32;

QY 8 RAYPGGLTVSGHPLATACAVATTNAMEDEGMVANAARIGEOVLGPGRLDLAARHRSVGEV 67  
DB 472 RAYAPLLARENAALTGAAGSPGAGA--DDEGVAAVAA-----AAPGERAVPAGYGAAGIL 524  
QY 68 RGLGVFWA-----GSDPER-----AGLR-----VEVLGAQCRRRDVGVA-- 101  
DB 525 AALGRLSAAPASPAGGDDPDAARHADDDAGRAAGRAVAVECLA-C--RGILEALAE 581  
QY 102 ---GDAAVV-GVLGPQRQHRARADGSSISALVASPP-----GQHTSIH 155  
DB 639 LMRLRGDLRVAGGSEAAVAVRAVSLVAGALGPRDPLRPLSPSSAAAAADLLFDNQSLR 698  
QY 156 PRSSNGSPVTHISQMNAASSGTSRSTLFRWQSCMTIPGSASSGLRESSQSASTCTDG 215  
DB 699 PLLAAASAPDAADALAAASAAAPREGKRKSPGPAPPPGGGGPPPKTKS----- 751  
QY 216 NDSGAGSDQLGFBGAQQRGKRRDRDVPAAQORPAVHPAGPAGPADRVGVDPGRHRRARG 275  
DB 752 ----GAD---APGSDA-----RAPLPAPAPPST--PPGPEPAP---AQPAAPRAAAA 791  
QY 276 QHQPRDGSQRQASRTVGVVPVSNVLSAGIRCTPTTTRAVAILCATLASKRGVVAOPAGD 335  
DB 792 QARPREVA-----VSRPAPGDPPLGGWR-RQP-----PGPSHT 824  
QY 336 VAAAAAGSPWPSVSVARVPVAVLTGPPRRPSDTGSIQVGRPAVLFAPE-----QRC 389  
DB 825 AAPAAAA-----LEAYCSPRAVAELTDHPLFPVP-----WRPALMFDPRALASTAARC 872  
QY 390 R--RRADQRSC-----RQHPGGGRHVQIVASARGTVEIGSIARLCGKDEAVAAALHYVA 441

```
Db      873  AGPAPAAQACGGDDDDNPHPHCAAGGRLFGPIRAS---GPLRRMAA-----WWR 920
QY      442  PVGEKQDYIDRALRNIGPYLPAEVPAIVGSIAATGPVPGTAWIVRQ--YFKLLRAKAN-- 497
Db      921  QIEDPED-----VRVVVLYSPLPGEDIAGGGASGGP---PENSAERGGLSCLIAALANRL 972
QY      498  -----WEDTWT 503
Db      973  CGPDTAAWAGNWT 985
```

Search completed: September 16, 2005, 20:55:54  
Job time : 49 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2005, 20:36:13 ; Search time 179 Seconds  
(without alignments)  
1570.567 Million cell updates/sec

Title: US-10-607-752-116  
Perfect score: 2862  
Sequence: 1 IYSTFADRAYPGGLTYSGHP.....IPSRARAEEIHGSHHHH 549

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	284	9.9	451	2 Q82ER2	Q82er2 streptomyc
2	273	9.5	451	2 Q9XA10	Q9xa10 streptomyc
3	202.5	7.1	469	2 Q8FN12	Q8fn12 corynebacte
4	185.5	6.5	608	2 Q9Q5K9	Q9q5k9 herpesvirus
5	182	6.4	1442	2 Q42066	Q42066 equid herpe
6	182	6.4	2087	2 Q8MXL2	Q8mxl2 leishmania
7	180	6.3	438	2 Q8NMX2	Q8nmx2 corynebacte
8	180	6.3	456	2 Q842J4	Q842j4 corynebacte
9	180	6.3	456	2 Q6M323	Q6m323 corynebacte
10	179.5	6.3	1408	2 Q6X125	Q6x125 bovine herp
11	179	6.3	1422	2 Q82D83	Q82d83 streptomyc
12	176.5	6.2	1461	1 I818_PRVIF	P11675 pseudorabie
13	174	6.1	3889	2 Q6SS58	Q6sse8 chlamydomon
14	173.5	6.1	1783	1 RAA3_CHLRE	Q9fec4 chlamydomon
15	172	6.0	1446	1 I818_PRVKA	P33479 pseudorabie
16	170	5.9	813	2 Q8GFF3	Q8gff3 streptomyc
17	169	5.9	775	1 ICF0_HHV11	P08393 human herpe
18	169	5.9	990	2 Q9BLV0	Q9blv0 leishmania
19	168	5.9	581	2 Q6H509	Q6h5q9 oryza sativ
20	168	5.9	816	2 Q7QWN8	Q7qwn8 giardia lam
21	167.5	5.9	579	2 Q8GFF2	Q8gff2 streptomyc
22	166	5.8	1733	1 VNUA_PRVKA	P33485 pseudorabie
23	165.5	5.8	2658	2 Q9GRU9	Q9gru9 leishmania
24	164.5	5.7	1479	2 Q82FF7	Q82ff7 streptomyc
25	164	5.7	865	2 Q62DN2	Q62dn2 burkholderi
26	163.5	5.7	2274	2 Q9Z1K7	Q9z1k7 mus musculu
27	162.5	5.7	1685	2 Q3UEW8	Q3uem8 homo sapien
28	162	5.7	382	2 Q8S0V8	Q8s0v8 oryza sativ
29	162	5.7	438	2 Q63JU4	Q63j14 burkholderi
30	161.5	5.6	1187	2 Q8P8Z4	Q8p8z4 xanthomonas
31	161	5.6	1345	2 Q9L060	Q9l060 streptomyc

32	160.5	5.6	2303	2	Q95996	Q95996 homo sapien
33	158	5.5	1454	2	Q8JL63	Q8jl63 suid herpes
34	157	5.5	1841	2	Q63VY6	Q63vy6 burkholderi
35	156.5	5.5	1958	2	Q89340	Q89340 suid herpes
36	156	5.5	821	2	Q8VPM9	Q8vpm9 micrococcus
37	156	5.5	1463	2	Q9ADP6	Q9adp6 streptomyc
38	156	5.5	2796	2	Q48926	Q48926 mycobacteri
39	154	5.4	1684	2	Q91LK9	Q91lk9 white spot
40	153.5	5.4	595	2	Q6YX66	Q6yx66 oryza sativ
41	153.5	5.4	1240	2	Q8DWH8	Q8dwh8 rat cytomeg
42	153	5.3	1014	2	Q9Y0K3	Q9y0k3 raietonia s
43	153	5.3	1111	2	Q9L0P1	Q9l0p1 streptomyc
44	153	5.3	1937	2	Q7W286	Q7w286 bordetella
45	152.5	5.3	730	2	Q06634	Q06634 bovine herp

## ALIGNMENTS

RESULT 1  
Q82ER2 PRELIMINARY; PRT; 451 AA.  
AC Q82ER2  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Putative aminotransferase.  
GN OrderedLocustNames=SAV4551;  
OS Streptomyces avermitilis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=33903;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680;  
RX MEDLINE=22698306; PubMed=12692562;  
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;  
RT "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";  
RL Nat. Biotechnol. 21:526-531(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
RT "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
CC -/- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent aminotransferase family.  
DR EMBL; AP005039; BAC72263.1; -.  
DR HSSP; P16932; 2DKB.  
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.  
DR GO; GO:0008483; F:transaminase activity; IEA.  
DR InterPro; IPR005814; Aminotrans\_3.  
DR Pfam; PF00202; Aminotran\_3; 1.  
DR PROSITE; PS00600; AA\_TRANSFER\_CLASS\_3; 1.  
KW Complete proteome; Pyridoxal phosphate.  
SQ SEQUENCE 451 AA; 48232 MW; 16BDCAS9B276F9CA CRC64;

Query Match 9.9%; Score 284; DB 2; Length 451;  
Best Local Similarity 45.9%; Pred. No. 2.3e-07;  
Matches 72; Conservative 20; Mismatches 35; Indels 30; Gaps 6;

Qy 1 IYSTFADRAYPGGLTYSGHPATACAVATINAMEDEGMVANAARIGEOVLGPGRLDLAAR 60

Db 298 IASTFGKRAYPGGLTYSGHPACAAATATINNVMAEEGVVENAANLGARVIEPGLRELAER 357

Qy 61 HRSVGEVGLGVFWAGSDPERAGLRVEVLGAQCRRRDV---GAGDA---AAVGVLGPG 113

```

Db 358 HPSVGEVGVGFVFA-----LELVKDRTEPLVPYNAGEANAPMAAFGA----- 403
Qy 114 RQHRARADG-----SISALVASPPRAASAPASIGL 145
Db 404 ---AAKANGLWPFINMRTHV-PPCNVTEAEKEGL 436

RESULT 2
ID Q9XA10 PRELIMINARY; PRT; 451 AA.
AC Q9XA10;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative aminotransferase.
GN ORFNames=SC66T3.33;
CN Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OX Streptomycineae; Streptomycetaceae; Streptomycetes.
NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL coelicolor A3(2).";
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
CC aminotransferase family.
DR EMBL; AL939117; CAB45489.1; -.
DR PIR; T35390; T35390.
DR HSSP; P16932; 2DKB.
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005814; Aminotrans_3.
DR Pfam; PF00202; Aminotran_3; 1.
DR PROSITE; PS00600; AA TRANSFER CLASS 3; 1.
KW Aminotransferase; Complete proteome; Pyridoxal phosphate; Transferase.
SQ SEQUENCE 451 AA; 48413 MW; 43CF2DD9AFA7E8AB CRC64;

Query Match 9.5%; Score 273; DB 2; Length 451;
Best Local Similarity 69.3%; Pred. No. 8.6e-07;
Matches 52; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 IYSTFADRAYPGGLTYSCHPLATACAVATINAMEDEGMVANARIGQVLGPGRLDLAAR 60
Db 298 IAAVFAERYPGGTYSCHPLAACAAVATINVMAEVGVHAARLGAEVVEPALRELAER 357
Qy 61 HRSVGEVRGLGVFWA 75
Db 358 HPSVGEVGVGFVFA 372

RESULT 3
ID Q8FN12 PRELIMINARY; PRT; 469 AA.
AC Q8FN12;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative aminotransferase.
GN OrderedLocusNames=CE2336;
CN

OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OX Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y8-314;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579(2003).
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
CC aminotransferase family.
DR EMBL; AP005222; BAC19146.1; -.
DR HSSP; P12995; 1QJ3.
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005814; Aminotrans_3.
DR Pfam; PF00202; Aminotran_3; 1.
DR PROSITE; PS00600; AA TRANSFER CLASS 3; UNKNOWN_1.
KW Aminotransferase; Complete proteome; Pyridoxal phosphate; Transferase.
SQ SEQUENCE 469 AA; 50166 MW; AFFA3E4482C29F79 CRC64;

Query Match 7.1%; Score 202.5; DB 2; Length 469;
Best Local Similarity 42.7%; Pred. No. 0.0045;
Matches 41; Conservative 15; Mismatches 27; Indels 13; Gaps 1;

Qy 1 IYSTFADRAYPGGLTYSCHPLATACAVATINAMEDEGMVANARIGQVLGPGRLDLAAR 60
Db 320 IRDTQAOYSGGLTYSCHPLAVAPALAAKVVYDEKIFERVASLGENLIGPLABIGQK 379
Qy 61 HRSVGEVRGLGVFW-----AGSDPERAG 83
Db 380 YAAVGVGVGIGFFWALEFVSDAQAKTPAGADAMAAG 415

RESULT 4
ID Q9Q5K9 PRELIMINARY; PRT; 608 AA.
AC Q9Q5K9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE NTR.
OS Herpesvirus papio.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
NCBI_TaxID=10394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Baboon lymphocryptovirus BA65;
RA Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,
RA Hayward G.S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF20364; AAF23950.1; -.
SQ SEQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;

Query Match 6.5%; Score 185.5; DB 2; Length 608;
Best Local Similarity 28.5%; Pred. No. 0.046;
Matches 109; Conservative 29; Mismatches 150; Indels 95; Gaps 22;

Qy 48 QVLGPGRLDLAARHRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRRRDVGAGDAAAV 107
Db 44 QVHGP-----RSPRIERRGSAQRGHPPPGAG-----QRPSGPTGGHPAAP 84
Qy 108 GVLGPQRQHRARADGSISSALVASPPRAASAPASIGLGPSSQHTSIHPRSSNGSPTVHI 167
Db 85 GAFGRSPRPTERRRG---SAQRGHPPPGAGQRPS-----GPTGGHP-----AATGAP---- 128

```

QY 168 SQMVAASGTSRRSSTLFRWQSPCMIPGSSAGLRESSQASSTCTDNDGSGAGSDOLGE 227  
D 129 ---GPRSPRTERRRGSAQRGHP---PG-----AGQPSGPTGHPAAGAPGPRS 173  
QY 228 PQAQORQKRDVPAQORPA---VHPAGPGPADRVGVDPG-----RHRRARGOHQ- 278  
D 174 PRTERRRGSAQRGHPGAGORPSGPTGHPAAGP-----PGPRSPRTERRRGSAQR 226  
QY 279 --PRDGSROASRTVSGVPVSNVLSAGIRC-RTPTTTRAVAICLATLASRGVAP---Q 331  
D 227 GHPPGAGQPSGPTGHPAAGP---APGRSPRTERRRG-----SAQRGHPGAGOR 277  
QY 332 PAGDV-ARAAAAGSWP---VRSVAPVAVLRTGPPP---RRPS-DTGSITQVGRPAVLFA 384  
D 278 PSPTGHPAAGAPGAPGPRSPRTERRRGSAQRGHPGAGORPSGPTG-----GHPAAGP 332  
QY 385 PEQRCRRADOR-SCRQIHGGG 406  
D 333 PGPRSPRTERRRGSAQRGHPGPPG 355

## BLT 5

QY 042066 PRELIMINARY; PRT; 1442 AA.  
AC 042066;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE 64.  
OS Equid herpesvirus 4.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Varicellovirus.  
OX NCBI\_taxID=10331;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NS80567;  
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;  
RT "The DNA sequence of equine herpesvirus-4."  
RL J. Gen. Virol. 79:1197-1203 (1998).  
DR EMBL; AF030027; AAC59583.1; -  
DR EMBL; AF030027; AAC59599.1; -  
DR PIR; T42607; T42607.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0016563; P:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR005205; Herpes\_ICP4\_C.  
DR InterPro; IPR005206; Herpes\_ICP4\_N.  
DR Pfam; PF03585; Herpes\_ICP4\_C; 1.  
DR Pfam; PF03584; Herpes\_ICP4\_N; 1.  
SEQUENCE 1442 AA; 151749 MW; CF50DB5372E47DC7 CRC64;

Query Match 6.4%; Score 182; DB 2; Length 1442;  
Best Local Similarity 21.4%; Pred. No. 0.17;  
Matches 136; Conservative 47; Mismatches 170; Indels 282; Gaps 28;

QY 5 PADRAYP-----GGLTSGHPLATACAVATINAMEDGMVANAARIGEQ----- 48  
D 542 YADWAYPRDDAGRODSHAAGVTASYPAQAQ-----ASQPDPPATSARVEEYTRV 594  
QY 49 -----VLGFGRLR---DLAARHRSVGEV-----RGLGVFWAGSDP 79  
D 595 CAALGPRKTAAGTGTTPKPTAFRLRELGDVCLACQAVFALLRLRGASAVPGLD 654  
QY 80 ER-----AGLREVLGAQC-----RRDVVG-----AGDAAAVGLGPGORQH- 116  
D 655 SEIPSPACPPALCSNPAGLET-----AALCALYELDLVERARLGLSDPTIHLGPDRL 710  
QY 117 -----PARADG-SISSALVASPPRAASSAPASIGLGPSQOHT 152  
D 711 AVRAVLVAVRTVAPLVYNAEGARASAWTITQAVFSIPSLAGMLGEAVL----- 763

QY 153 SIHPRSSNGSPTV--HISQSNMAASSGTSRRSSTLFRWQS-----PCMIPGS-----ASSGL 202  
D 764 -LAPPRSQSSSSGVDGVOQSSLSSESGSQTSRIPALWPTVPGKPLVVPATSHSQSSSPQ 822  
QY 203 RESSQASSTCTDNDGSA-----GSDQLGEPGAQ----- 232  
D 823 HQSSGSGPTTSRATQTQARPSGQKARSPPAASQAILQEMPVSSQGGGPPAPYASPNDRP 882  
QY 233 ---RQRCKHRRDRDVPQAQRPVHPAGPGPADRVGVDPGRRRARGOHQPDGSDRASR 289  
D 883 VNGRPGSKGKRSEPLE--PA---AGELPGSGGYDPVAPVESPPAPKRVGT--QAPR 935  
QY 290 TVSGVPVSNVLSAGIR-----CRTPTRAVAICLATLASRGVVAQPADGVARAAAAG 343  
D 936 ALGPMPPGPHRRGGFRFVPHGDCTP-----PPCDSARAAYC- 973  
QY 344 SPWPVRSVAPVAVLRTGPPRRPSDTGSITQVGRPAVLFAPEQRCCRRAQRSCROIHP 403  
D 974 ---PPELVAEILI-----DHPLFPEARWPAITFDPO----- 1000  
QY 404 GGGHRHVOIVASARCTVEIGSIARLCGKDEAVALHYVAVGCEKQDIYDRALNIGPYLPA 463  
D 1001 -----ALATIARCN-----GP--PA 1014  
QY 464 EVPALVGSIAATGVPGTAWIVRQYPKLRAKANW 498  
D 1015 REGARFCELAASGP-----LRRRAAM 1035

## RESULT 6

Q8MXL2 PRELIMINARY; PRT; 2087 AA.  
AC Q8MXL2;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=Chr3\_0240;  
OS Leishmania major.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_taxID=5664;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Friedlin;  
RA MEDLINE=22738071; PubMed=12853638; DOI=10.1093/nar/gkg469;  
RA Worthey E.A., Martinez-Calvillo S., Schnauer A., Aggarwal G.,  
RA Cawthra J., Fazelinia G., Fong C., Fu G., Hassebrock M., Hixson G.,  
RA Ivens A.C., Kiser P., Marsolini F., Rickell E., Salavati R., Sisk E.,  
RA Sunkin S.M., Stuart K.D., Myler P.J.;  
RT "Leishmania major chromosome 3 contains two long convergent  
polycistronic gene clusters separated by a tRNA gene."  
RL Nucleic Acids Res. 31:4201-4210(2003).  
DR EMBL; AC125735; AAM68997.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 2087 AA; 213463 MW; 5941B10021775F1B CRC64;

Query Match 6.4%; Score 182; DB 2; Length 2087;  
Best Local Similarity 22.9%; Pred. No. 0.24;  
Matches 152; Conservative 65; Mismatches 244; Indels 204; Gaps 36;

QY 16 YSGHPLATACAVATINAMEDGMV-----ANAAIRGEQVLGFLGLDLAARHS----- 63  
D 141 YGRQPOQPSGQAVGAHREDGEVNGSDAHDRELSEQ-----LCSRTTSCRTSPWS 193  
QY 64 -GVEVRGLGVFWAGSDP-----BRAGLRVVELGAQ-CRRDVGAGDAAAVGLGPO 113  
D 194 HVNRPPALG---GSSNSHSDGVDYRAAAASSELHSQRCRRHRSRYTQSDV----- 243  
QY 114 ROHRAR-ADGSISSALVASPPRAASSAPA-SIGLGPSQOHTSIHPRSSNGSPVHISQM 171  
D 244 --HRLHGADAPASSSLESTAPVDTSAATAAAGAAKGNERRDDAPTHSTGSHRHQSP 301  
QY 172 NA-ASSGT-----SRRSSTLFRWQSP-----C-MIPGSASSG-----LRESSQS 208



Qy	RL	RN	RP	RC	RA	RD	RE	RF	RG	RH	RI	RJ	RK	RL	RM	RN	RO	RP	RS	RT	RU	RV	RW	RX	RY	RZ	SA	SB	SC	SD	SE	SF	SG	SH	SI	SJ	SK	SL	SM	SN	SO	SP	SQ	SR	SS	ST	SV	SW	SX	SY	SZ	TA	TB	TC	TD	TE	TF	TG	TH	TI	TJ	TK	TL	TM	TN	TO	TP	TP	TR	TS	TT	TU	TV	TW	TX	TY	TZ	UA	UB	UC	UD	UE	UF	UG	UH	UI	UJ	UK	UL	UM	UN	UO	UP	UQ	UR	US	UT	UU	UV	UW	UX	UY	UZ	VA	VB	VC	VD	VE	VF	VG	VH	VI	VJ	VK	VL	VM	VN	VO	VP	VQ	VR	VS	VT	VU	VV	UV	VW	VX	VY	VZ	WA	WB	WC	WD	WE	WF	WG	WH	WI	WJ	WK	WL	WM	WN	WO	WP	WQ	WR	WS	WT	WU	WV	WW	WX	WY	WZ	XA	XB	XC	XD	XE	XF	YG	YH	YI	YJ	YK	YL	YM	YN	YO	YP	YQ	YR	YS	YT	YU	YV	YW	YX	YY	YZ	ZA	ZB	ZC	ZD	ZE	ZF	ZG	ZH	ZI	ZJ	ZK	ZL	ZM	ZN	ZO	ZP	ZQ	ZR	ZS	ZT	ZU	ZV	ZW	ZX	ZY	ZZ	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ	BA	BB	BC	BD	BE	BF	BG	BH	BI	BJ	BK	BL	BM	BN	BO	BP	BQ	BR	BS	BT	BU	BV	BW	BX	BY	BZ	CA	CB	CC	CD	CE	CF	CG	CH	CI	CJ	CK	CL	CM	CN	CO	CP	CQ	CR	CS	CT	CU	CV	CW	CX	CY	CZ	DA	DB	DC	DD	DE	DF	DG	DH	DI	DJ	DK	DL	DM	DN	DO	DP	DQ	DR	DS	DT	DU	DV	DW	DX	DY	DZ	EA	EB	EC	ED	EE	EF	EG	EH	EI	EJ	EK	EL	EM	EN	EO	EP	EQ	ER	ES	ET	EU	EV	EW	EX	EY	EZ	FA	FB	FC	FD	FE	FF	FG	FH	FI	FJ	FK	FL	FM	FN	FO	FP	FQ	FR	FS	FT	FU	FV	FW	FX	FY	FZ	GA	GB	GC	GD	GE	GF	GG	GH	GI	GJ	GK	GL	GM	GN	GO	GP	GQ	GR	GS	GT	GU	GV	GW	GX	GY	GZ	HA	HB	HC	HD	HE	HF	HG	HH	HI	HJ	HK	HL	HM	HN	HO	HP	HQ	HR	HS	HT	HU	HV	HW	HX	HY	HZ	IA	IB	IC	ID	IE	IF	IG	IH	II	IJ	IK	IL	IM	IN	IO	IP	IQ	IR	IS	IT	IU	IV	IW	IX	IY	IZ	JA	JB	JC	JD	JE	JF	JG	JH	JI	IJ	JK	JL	JM	JN	JO	JP	JQ	JR	JS	JT	JU	JV	JW	JX	JY	JZ	KA	KB	KC	KD	KE	KF	KG	KH	KI	KJ	KL	KM	KN	KO	KP	KQ	KR	KS	KT	KU	KV	KW	KX	KY	KZ	LA	LB	LC	LD	LE	LF	LG	LH	LI	LJ	LK	LL	LM	LN	LO	LP	LQ	LR	LS	LT	LU	LV	LW	LX	LY	LZ	MA	MB	MC	MD	ME	MF	MG	MH	MI	MJ	MK	ML	MM	MN	MO	MP	MQ	MR	MS	MT	MU	MV	MW	MX	MY	MZ	NA	NB	NC	ND	NE	NF	NG	NH	NI	NJ	NK	NL	NM	NN	NO	NP	NQ	NR	NS	NT	NU	NV	NW	NX	NY	NZ	OA	OB	OC	OD	OE	OF	OG	OH	OI
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----



```
QY 334 GDVARA-----AAAGSPWVRVSARP-----VAVLRGTPPPRRPSDGTSGITQVGRP 379
Db 439 ASSASATSSAAASAPAPAPAPRRKRSTNNHLSLMADGPP---PTDGLPLTLPLGEP 495
QY 380 AVLFAPEORCRRRA-----DQSCROIHGGGRHVQIVASAGTV-----EIGS 423
Db 496 WFGSDPPADGRVRYGGAGDSREGLWDEDDVRQ---AAARY-----RAAAGPVPVFIPEMGD 548
QY 424 IARLCGKDEAAALHYVAPVGEKQDYID-----RALRNI GPYLPAP 464
Db 549 SRK-----QHEALVRLYSAGAEAMSWLQNPROMQADQRFQCORRVHAPHGHSFITGS 605
QY 465 V-----PALVGSIAATGPVGTAWIVROYPKLLRAKANWEDTWTFFSIEEKEHPRGSVAGP 520
Db 606 VTPPLPHIGDAMAAQDPL-----WALPHA VASAVMSRRYDRTKTQKFIQLSLRAVADMAYP 661
QY 521 VFRVNLGRAIPSRARA 537
Db 662 -----GRAADPRAGEA 672

RESULT 13
ID Q6SSE8 PRELIMINARY; PRT; 3889 AA.
AC Q6SSE8;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Minus agglutinin.
GN Name=SAD1;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=CC-621;
RA Ferris P.J., Waffenschmidt S., Umen J.G., Ishida K., Kubo T., Lau J.,
RA Goodenough U.W.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY450929; AAS07042.1;
DR GO; GO:0005199; F:structural constituent of cell wall; IEA.
DR InterPro; IPR003882; Pistil extensin.
DR PRINTS; PR01218; PSTLEXTENSIN.
DR TIGRFAMs; TIGR01414; autotrans barl; 1.
SQ SEQUENCE 3889 AA; 389223 MW; 4DE5B44D5507214A CRC64;

Query Match
Best Local Similarity 24.2%; Pred. No. 1.2; Length 3889;
Matches 116; Conservative 49; Mismatches 190; Indels 124; Gaps 22;

QY 33 MEDEGMVANAARIGEVQLGGLRLDAKRRSVGEVGLGVFWAGSDPERAGLRYEVLGAQ 92
Db 2802 MEDE-----AAATRIQDAAADPAVEANRSRRKQAGSV-----EEQVAINPAVPRAS 2849
QY 93 CRRDVRVCGAAGAAVGLGPRQRRARADGSGISSALVALSPPRAASSAPASIGLPGSQHT 152
Db 2850 VLERPDAVAAALAAVA-----ASGAPPGQTGPLPITTEATGEN---GLGSS----- 2892
QY 153 SIHPRSSNGSPVHTISQSMNAASCTSRSSSTLFRWQS--PCWIPGSSAGSLRESSOSAS 210
Db 2893 ---PRDGRVWTTASVSHGRD-----TSKLLHPMARPSRLGASLVPASATT-----NGSGN 2940
QY 211 TCTDNGDSGAGSDOLGEPGAQQRGKRRDRDVPAAQRPVHPAGPGPADRVGVDPGRH 270.
Db 2941 SSGNGRESSGSGTSGAPAMPREP-----VGGAPSNASAAAAA-----AQPAAH 2991
QY 271 RRARGQHOPRGSQRQASRTVSGVFPVSNVLASGIRCKTPPTTRVAICLATLASR-GVWA 329
Db 2992 QDLFG-----ELDTTTLTTSKMTADAGAAAPPNLPSPMWR-----LGSRLGLVR 3035
QY 330 PQAGDVARAAAAGSPWVRVSARPVAVLRGTPPPRRPSDGTSGITQVGRPAVLPAPBQRC 389
```

```
Db 3036 GGSNSGAQVAPA-SPLPAKAPSPAAAARPP-----GAVTT--NAAVPMPPQKV 3085
QY 390 RRR-----ADQSCROIHP-----GGGRH-----VOIVASARGTVEIGSIARLCGKDE 432
Db 3086 FRSPSEFANRAQGAAPPAAPAAAANGGRELKQOPAVQAVSSTTSIRSNS-----SGSGN 3141
QY 433 AVAALHYVAPVGEKQDYIDRALRNIGPVLPAEVPAALVGSIA-----ATGPVPGTAW 483
Db 3142 PLA-----RALRYMSVPKPGAQSTASNAAPAAAEAPAPPSRHTAW 3184

RESULT 14
ID _RAA3 CHLRE STANDARD; PRT; 1783 AA.
AC Q9FEC4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Trans-splicing factor Raa3, chloroplast precursor.
GN Name=RAA3;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN 1;
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=137c / CC-125;
RX MEDLINE=21181833; PubMed=11285239; DOI=10.1093/emboj/20.7.1765;
RA Rivier C., Goldschmidt-Clermont M., Rochaix J.-D.;
RT "Identification of an RNA-protein complex involved in chloroplast
RT group II intron trans-splicing in Chlamydomonas reinhardtii.";
RL EMBO J. 20:1765-1773(2001).
CC -!- FUNCTION: Required for trans-splicing of exons 1 and 2 of the
CC chloroplast encoded psaa mRNA (a group II intron). May be required
CC for stability of the chloroplast RNA-protein complex in which it
CC is found.
CC -!- SUBUNIT: Part of a 1700 kDa complex that includes the precursor
CC RNA to exon 1 and the tscA RNA.
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma.
CC -!- DOMAIN: The N-terminal 453 amino acids are dispensable, while the
CC C-terminal 630 amino acids are required for function.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF310675; AAG40000.1;
CC EMBL; AF310674; AAG39999.1;
CC DR Chloroplast; mRNA processing; mRNA splicing; Transit peptide.
CC KW TRANSIT 1 40 Chloroplast (Potential).
CC FT CHAIN 41 1783 Trans-splicing factor Raa3.
CC FT DOMAIN 112 311 Ala-rich.
CC FT DOMAIN 343 436 Ser-rich.
CC FT DOMAIN 478 1078 Ala-rich.
CC FT DOMAIN 1310 1415 Ala-rich.
CC FT DOMAIN 1416 1430 Gln-rich.
CC FT DOMAIN 1496 1506 Arg-rich.
CC FT DOMAIN 1678 1722 Ala-rich.
CC FT DOMAIN 771 778 Poly-Ala.
CC FT DOMAIN 920 926 Poly-Pro.
CC FT DOMAIN 927 932 Poly-Ala.
CC FT DOMAIN 1047 1055 Poly-Gly.
CC FT DOMAIN 1318 1325 Poly-Ala.
CC FT DOMAIN 1405 1415 Poly-Ala.
CC FT DOMAIN 1669 1675 Poly-Pro.
CC SQ SEQUENCE 1783 AA; 180399 MW; 40F6206BAGEBDCDB CRC64;

Query Match
6.1%; Score 173.5; DB 1; Length 1783;
```

```
Best Local Similarity 21.1%; Pred. No. 0.57;
Matches 127; Conservative 64; Mismatches 235; Indels 177; Gaps 22;

QY 13 GLTSGHPLATACAVATINAMEDSGMVANAARIGEVLPGLRLDLAARHRS-----VGEV 67
D 118 QOARHRRQMAAATTVSAAPQTGATKPAATAKTTQPRGSDADAGSAQSQYGFDP 177
QY 68 RGLGVF-----WAGSDPERAGLVEVLGAQC--RRRDVVG-----AGDAAVG 108
D 178 PGGALKAVDAADADPADVAASGAPAGISDQLSTPACPPERPQAGKPRASGRAPAP 237
QY 109 VLGPQ-----RQHRARA-DGSI-----SALVAPPPRAASSAP 140
D 238 GVGFQDVGGSGACAPAPDESHMGLTHRDQGHDERISQTAGEAWKAGAVAPPAITPSP 297
QY 141 ASIGLGP-----SQGHTSIH 155
D 298 PGLAAAPTRLASSALGTHSSDGMRRVAPVGRDTPSLSAVAGPVTLSGSSSSSGRNSN 357
QY 156 PRSNGSPTVHISQSMNAASGTS-----RRSSTLFRWQS-----PC 192
D 358 SNTSTSTSGVTITTSNVGNGASPOERLMAARAVVTMNTHLGRRGRSPAPLPTGGM 417
QY 193 MIPGASSGLRESQSASTCTDGNDSGAGSD-OLGEPGAQORQRKRRDRDVPACORPA 251
D 418 SIATSAASSSTSSASSSSMNDGNAKTSDAVSLPVGQ-----PAEQPH 465
QY 252 VHPAGPADRVGVDPGHRRRARGQHOPRQDSDQASRTVSG-----VPVESNLS 302
D 466 V-PTAPGPGSQTGAS-----AVAAQAPSSAMPTAAMAATMGSAITGSAATLPTAAVSS 518
QY 303 AGICRPTTTTAVAILCLATLASRGVAPQAGDVARAAAAGSPWPSVARPVAVLETGP 362
D 519 AAEGTQPSGULLAGGRPALLGRTI-----QGRITARLOAAREALRAARHARVGAAMQPPP 573
QY 363 PPRRP--SDTGSITQVGRPAVLFAPEQRCRRRARDQSCRTQHPGGRHVQIVASARGTVE 420
D 574 VQARPVQSGSQVQVQGVQSPG--RRQEPAAATKLHVADGLPARPVQPAVSATD 630
QY 421 IGSTARLCGKDEAAVLAHYVAPVEKEQDYIDRALRNLGNPLPAEVPALVGSIA-ATGVPV 479
D 631 LQT-----DTATAA-SAPFPVSD-----ASLGSTELAASAPTTSLASASGPAI 673
QY 480 GTA 482
D 674 GTS 676

RESULT 15
ID IE18 PRVKA STANDARD; PRT; 1446 AA.
AC P33479;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Immediate-early protein IE180.
GN Name=IE;
OS Pseudorabies virus (strain Kaplan) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=33703;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021039; PubMed=2171211;
RA Virec C., Kosmik Z., Paces V., Schirm S., Schwyzler M.;
RT "Pseudorabies virus immediate-early gene overlaps with an oppositely
RT oriented open reading frame: characterization of their promoter and
RT enhancer regions."
RL Virology 179:365-377 (1990).
CC -!- FUNCTION: This IE protein is a multifunctional protein capable of
CC migrating to the nucleus, binding to DNA, trans-activating other
CC viral genes, and autoregulating its own synthesis.
CC -!- SUBCELLULAR LOCATION: Nucleus of infected cells.
```

Db	610	DPL----	WALPHA	SAVAMS	REYDR	TQKTF	ILQSL	RRAYAD	WAYP-----	GRAADPRAG	659
Qy	536	RA	537								
Db	660	EA	661								

Search completed: September 16, 2005, 20:52:08  
Job time : 184 secs

This Page Blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2005, 20:27:42 ; Search time 25 Seconds  
(without alignments)  
1639.293 Million cell updates/sec

Title: US-10-607-752-116  
Perfect score: 2862  
Sequence: 1 IYSTFADRAYPGGLTYSVGH...IPSRARAAEIHGSHHHHH 549

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2862	100.0	582	3	US-09-450-072-81
2	2862	100.0	582	4	US-09-351-348-81
3	2145	74.9	582	3	US-09-450-072-80
4	2145	74.9	582	4	US-09-351-348-80
5	1906	66.6	582	3	US-09-450-072-79
6	1906	66.6	582	4	US-09-450-072-79
7	490	17.1	97	3	US-09-450-072-71
8	490	17.1	97	4	US-09-351-348-71
9	440	15.4	87	3	US-09-450-072-74
10	440	15.4	87	4	US-09-351-348-74
11	389	13.6	75	3	US-09-450-072-70
12	389	13.6	75	4	US-09-351-348-70
13	373	13.0	70	3	US-09-450-072-69
14	373	13.0	70	4	US-09-351-348-69
15	326	11.4	59	3	US-09-450-072-77
16	326	11.4	59	4	US-09-351-348-77
17	255	8.9	49	3	US-09-450-072-72
18	255	8.9	49	4	US-09-351-348-72
19	237	8.3	46	3	US-09-450-072-73
20	237	8.3	46	4	US-09-351-348-73
21	224	7.8	44	3	US-09-450-072-76
22	224	7.8	44	4	US-09-351-348-76
23	222	7.8	456	4	US-09-489-039A-13165
24	206	7.2	38	3	US-09-450-072-67
25	206	7.2	38	4	US-09-351-348-67
26	204.5	7.1	819	4	US-09-252-991A-19569
27	196.5	6.9	606	4	US-09-252-991A-18233

28	196	6.8	613	4	US-09-252-991A-22424	Sequence 22424, A
29	194	6.8	973	4	US-09-252-991A-21386	Sequence 21386, A
30	192	6.7	802	4	US-09-252-991A-25050	Sequence 25050, A
31	191.5	6.7	672	4	US-09-252-991A-16941	Sequence 16941, A
32	191.5	6.7	1037	4	US-09-252-991A-25361	Sequence 25361, A
33	190.5	6.7	618	4	US-09-252-991A-23373	Sequence 23373, A
34	190.5	6.7	957	4	US-09-252-991A-20408	Sequence 20408, A
35	189.5	6.6	588	4	US-09-252-991A-30690	Sequence 30690, A
36	186	6.5	726	4	US-09-252-991A-20675	Sequence 20675, A
37	185	6.5	1246	4	US-09-252-991A-23140	Sequence 23140, A
38	180.5	6.3	412	4	US-09-252-991A-23193	Sequence 23193, A
39	180.5	6.3	822	4	US-09-252-991A-22479	Sequence 22479, A
40	180.5	6.3	1706	4	US-09-252-991A-31760	Sequence 31760, A
41	180	6.3	757	4	US-09-252-991A-23569	Sequence 23569, A
42	179	6.3	32	3	US-09-450-072-65	Sequence 65, Appl
43	179	6.3	32	4	US-09-351-348-65	Sequence 65, Appl
44	178.5	6.2	420	4	US-09-252-991A-20033	Sequence 20033, A
45	177.5	6.2	703	4	US-09-252-991A-31954	Sequence 31954, A

ALIGNMENTS

RESULT 1  
US-09-450-072-81

; Sequence 81, Application US/09450072  
; Patent No. 6358734  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; FILE REFERENCE: 11000.1042c1  
; CURRENT APPLICATION NUMBER: US/09/450,072  
; CURRENT FILING DATE: 1999-11-29  
; EARLIER APPLICATION NUMBER: 09/351,348  
; EARLIER FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 81  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-450-072-81

Query Match	100.0%	Score 2862;	DB 3;	Length 582;
Best Local Similarity	100.0%	Pred. No. 4.9e-241;		
Matches 549;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1	IYSTFADRAYPGGLTYSVGHPLATACAVATINAMEDGVANAARIGEQLGFLDLAAR	60	
Db	34	IYSTFADRAYPGGLTYSVGHPLATACAVATINAMEDGVANAARIGEQLGFLDLAAR	93	
Oy	61	HRSGVEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAVAAGVLPQQRHARA	120	
Db	94	HRSGVEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAVAAGVLPQQRHARA	153	
Oy	121	DGSISSALVAPPPRAASSAPASIGLGPSSQHTSIHPRSSNGSPVTHISQSNNAASSGTSR	180	
Db	154	DGSISSALVAPPPRAASSAPASIGLGPSSQHTSIHPRSSNGSPVTHISQSNNAASSGTSR	213	
Oy	181	RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQGEFGAQRQRKHDR	240	
Db	214	RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQGEFGAQRQRKHDR	273	
Oy	241	RDDVPAQRPAVHAGPGPADRVGVDPGRHRRARQHQPRGSDRQASRTYSGVPVSNV	300	
Db	274	RDDVPAQRPAVHAGPGPADRVGVDPGRHRRARQHQPRGSDRQASRTYSGVPVSNV	333	
Oy	301	LSAGIRCKTPTTTRAVAICLATLASRGVVVAPOPAGDVARAAAAGSPVRSVARPVAVLRT	360	
Db	334	LSAGIRCKTPTTTRAVAICLATLASRGVVVAPOPAGDVARAAAAGSPVRSVARPVAVLRT	393	

Qy 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 420  
Db 394 GPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 453  
Qy 421 IGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNI GPYLP AEVPALVGSIAATGPVPG 480  
Db 454 IGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNI GPYLP AEVPALVGSIAATGPVPG 513  
Qy 481 TAWIVROYPKLLRAKANWEDTWPFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 540  
Db 514 TAWIVROYPKLLRAKANWEDTWPFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 573  
Qy 541 HGSHHHHH 549  
Db 574 HGSHHHHH 582

RESULT 2  
US-09-351-348-81  
; Sequence 81, Application US/09351348  
; Patent No. 6436898  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; TITLE OF INVENTION: Of Mycobacterial Infections with Multi-Epitope Vaccines  
; FILE REFERENCE: 11000.1042  
; CURRENT APPLICATION NUMBER: US/09/351.348  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 81  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab

US-09-351-348-81

Query Match 100.0%; Score 2862; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 4.9e-241;  
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYSTFADRAYPGGLTYSCHPLATACAVATINAMEDEGMVANAARIGEOVLGPGLDLAAR 60  
34 IYSTFADRAYPGGLTYSCHPLATACAVATINAMEDEGMVANAARIGEOVLGPGLDLAAR 93  
Qy 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRERDVVGAGDAAAVGLGPQRHARA 120  
94 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRERDVVGAGDAAAVGLGPQRHARA 153  
Qy 121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
154 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 213  
Qy 181 RSSTLFRWQSPCMTPGSASSGLRESSQSASTCTDNDGSGSDQLGEPGAQRQRKH RD 240  
214 RSSTLFRWQSPCMTPGSASSGLRESSQSASTCTDNDGSGSDQLGEPGAQRQRKH RD 273  
Qy 241 RRDVPAQQRPAVHPAGPADRVGDPGRHRRARGQHOPRQSGDRQASRTVSGVPVESNV 300  
274 RRDVPAQQRPAVHPAGPADRVGDPGRHRRARGQHOPRQSGDRQASRTVSGVPVESNV 333  
Qy 301 LSAGIRCTPTTTRAVAI CLATLASRGVVAPOPAGDVARAAAAGSPWVRVARPVAVLRT 360  
334 LSAGIRCTPTTTRAVAI CLATLASRGVVAPOPAGDVARAAAAGSPWVRVARPVAVLRT 393  
Qy 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 420  
Db 394 GPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 453  
Qy 421 IGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNI GPYLP AEVPALVGSIAATGPVPG 480

Db 454 IGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNI GPYLP AEVPALVGSIAATGPVPG 513  
Qy 481 TAWIVROYPKLLRAKANWEDTWPFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 540  
Db 514 TAWIVROYPKLLRAKANWEDTWPFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 573  
Qy 541 HGSHHHHH 549  
Db 574 HGSHHHHH 582

RESULT 3  
US-09-450-072-80  
; Sequence 80, Application US/09450072  
; Patent No. 6358734  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders  
; TITLE OF INVENTION: and Methods for Their Use  
; FILE REFERENCE: 11000.1042c1  
; CURRENT APPLICATION NUMBER: US/09/450.072  
; CURRENT FILING DATE: 1999-11-29  
; EARLIER APPLICATION NUMBER: 09/351.348  
; EARLIER FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 80  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab

US-09-450-072-80

Query Match 74.9%; Score 2145; DB 3; Length 582;  
Best Local Similarity 67.4%; Pred. No. 1.6e-178;  
Matches 442; Conservative 0; Mismatches 0; Indels 214; Gaps 4;

Qy 1 IYSTFADRAYPGGLTYSCHPLATACAVATINAMEDEGMVANAARIGEOVLGPGLDLAAR 60  
34 IYSTFADRAYPGGLTYSCHPLATACAVATINAMEDEGMVANAARIGEOVLGPGLDLAAR 93  
Qy 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRERDVVGAGDAAAVGLGPQRHARA 120  
94 HRSVGEVRGLGVFWA----- 108  
Qy 121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
109 -GSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 167  
Qy 181 RSSTLFRWQSPCMTPGSASSGLRESSQSASTCTDNDGSGSDQLGEPGAQRQRKH RD 240  
168 RSSTLFRWQSPCMTPGSASSGLRESSQSASTCTDNDGSGA----- 207  
Qy 241 RRDVPAQQRPAVHPAGPADRVGDPGRHRRARGQHOPRQSGDRQASRTVSGVPVESNV 300  
208 -----GSDRQASRTVSGVPVESNV 226  
Qy 301 LSAGIRCTPTTTRAVAI CLATLASRGVVAPOPAGDVARAAAAGSPWVRVARPVAVLRT 360  
227 LSAGIRCTPTTTRAVAI CLATLASRGVVAPOPAGDVARAAAAGSPWVRVARPVAVLRT 286  
Qy 361 GPPRRPSDT----- 370  
287 GPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTV 346  
371 -----GSTITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTV 419  
347 RRARGQHOPRQSGTITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTV 406  
Qy 420 EIGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNI GPYLP AEVPALV----- 469  
407 EIGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNI GPYLP AEVPALVGS DPERAGLR 466

QY 470 -----GSIAATGVPCTAWIVROYPKLLR 493  
DB 467 VEVLGAQCRRRDVVAGDAAAVGLGQHRARADGSIATGVPCTAWIVROYPKLLR 526  
QY 494 AKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARAABHSHHHH 549  
DB 527 AKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARAABHSHHHH 582

RESULT 5  
US-09-450-072-79  
; Sequence 79, Application US/09450072  
; Patent No. 6358734  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder  
; FILE REFERENCE: 11000.1042c1  
; CURRENT APPLICATION NUMBER: US/09/450,072  
; CURRENT FILING DATE: 1999-11-29  
; EARLIER APPLICATION NUMBER: 09/351,348  
; EARLIER FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 79  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-351-348-80

Query Match 74.9%; Score 2145; DB 4; Length 582;  
Best Local Similarity 67.4%; Pred. No. 1.6e-178;  
Matches 442; Conservative 0; Mismatches 0; Indels 214; Gaps 4;

QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLPGLDLAAR 60  
DB 34 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLPGLDLAAR 93  
QY 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRRRDVVAGDAAAVGLGQHRARA 120  
DB 94 HRSVGEVRLGVFWA----- 108  
QY 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPTVHISQSMNAASGTSR 180  
DB 109 -GSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPTVHISQSMNAASGTSR 167  
QY 181 RSSTLFRWQSPCMIPGSASSGLRESQSASTCTDGNDSGAGSDQLGEPGAQQRQKRD 240  
DB 168 RSSTLFRWQSPCMIPGSASSGLRESQSASTCTDGNDSGA----- 207  
QY 241 RRDVPAQQRPAVHPAGPGPADRVGDPGRHRRARQHQPRDGSDRQASRTVSGVPESNV 300  
DB 208 -----GSDRQASRTVSGVPESNV 226  
QY 301 LSAGIRCRTPPTTRAVAI CLATLASRGVAPQAGDVARAAAAGSPWVRVARPVAVLRT 360  
DB 227 LSAGIRCRTPPTTRAVAI CLATLASRGVAPQAGDVARAAAAGSPWVRVARPVAVLRT 286  
QY 361 GPPRRPSDT----- 370  
DB 287 GPPRRPSDTGSDQLGEPGAQQRQKRDVDPQAQRPAVHPAGPGPADRVGDPGRH 346  
QY 371 -----GSIITQVGPVAVLFAPEQRCRRADORSCTHPCGGGRHVQIVASARGTV 419  
DB 347 RRARQHQPRDGSITQVGRPAVLFAPQRCRRADORSCTHPCGGGRHVQIVASARGTV 406  
QY 420 EIGSIALRCGKDEAAVAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALV----- 469  
DB 407 EIGSIALRCGKDEAAVAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSDDPERAGLR 466  
QY 470 -----GSIAATGVPCTAWIVROYPKLLR 493

DB 467 VEVLGAQCRRRDVVAGDAAAVGLGQHRARADGSIATGVPCTAWIVROYPKLLR 526  
QY 494 AKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARAABHSHHHH 549  
DB 527 AKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARAABHSHHHH 582

RESULT 5  
US-09-450-072-79  
; Sequence 79, Application US/09450072  
; Patent No. 6358734  
; GENERAL INFORMATION:  
; APPLICANT: Delcayre, Alain  
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder  
; FILE REFERENCE: 11000.1042c1  
; CURRENT APPLICATION NUMBER: US/09/450,072  
; CURRENT FILING DATE: 1999-11-29  
; EARLIER APPLICATION NUMBER: 09/351,348  
; EARLIER FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 79  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-450-072-79

Query Match 66.6%; Score 1906; DB 3; Length 582;  
Best Local Similarity 57.1%; Pred. No. 1.1e-157;  
Matches 399; Conservative 0; Mismatches 0; Indels 300; Gaps 2;

QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLPGLDLAAR 60  
DB 34 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLPGLDLAAR 93  
QY 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRRRDVVAGDAAAVGLGQHRARA 120  
DB 94 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRRRDVVAGDAAAVGLGQHRARA 153  
QY 121 ----- 120  
DB 154 DGSDRQASRTVSGVPESNVLSAGIRCRCTPTTRAVAI CLATLASRGVAPQAGDVARAA 213  
QY 121 ----- 120  
DB 214 AAGSPWVRVARPVAVLRTGTPPPRRPDSGTGDLGEPGAQQRQKRDVDPQAQR 273  
QY 121 -----DGSISSALVASPPRAASAPASIGLPGSQ 150  
DB 274 AVHPAGPGPADRVGDPGRHRRARQHQPRDGSISSALVASPPRAASAPASIGLPGSQ 333  
QY 151 HTSIHPRSSNGSPTVHISQSMNAASGTSRSTLFRWQSPCMIPGSASSGLRESQSAS 210  
DB 334 HTSIHPRSSNGSPTVHISQSMNAASGTSRSTLFRWQSPCMIPGSASSGLRESQSAS 393  
QY 211 TCTDGNDSGAGSDQLGEPGAQQRQKRDVDPQAQRPAVHPAGPGPADRVGDPGRH 270  
DB 394 TCTDGNDSGA----- 403  
QY 271 RRARQHQPRDGSDRQASRTVSGVPESNVLSAGIRCRCTPTTRAVAI CLATLASRGVAP 330  
DB 404 ----- 403  
QY 331 QPAGDVARAAAAGSPWVRVARPVAVLRTGTPPPRRPDSGTITQVGRPAVLFAPQRCR 390  
DB 404 -----GSIITQVGRPAVLFAPQRCR 423  
QY 391 RRADORSCTHPCGGGRHVQIVASARGTV EIGSIALRCGKDEAAVAALHYVAPVGEKQYI 450  
DB 424 RRADORSCTHPCGGGRHVQIVASARGTV EIGSIALRCGKDEAAVAALHYVAPVGEKQYI 483



```
Db 61 TLFRTWSPICPGSASSGLRESSQSASTCTDGNDSGA 97
|||||
RESULT 9
US-09-450-072-74
; Sequence 74, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT FILING DATE: 1999-11-29
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-450-072-74
Query Match 15.4%; Score 440; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 5.2e-31;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 284 DRQASRTVSGVPVSVNLVSGIRGRCRPTTTRAVAIATLASRGVVAPOAGDVAAAAAG 343
Db 1 DRQASRTVSGVPVSVNLVSGIRGRCRPTTTRAVAIATLASRGVVAPOAGDVAAAAAG 60
QY 344 SPWPVRSVARPVAVLRTGPPRRPSDT 370
Db 61 SPWPVRSVARPVAVLRTGPPRRPSDT 87
RESULT 10
US-09-351-348-74
; Sequence 74, Application US/09351348
; Patent No. 6436898
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; FILE REFERENCE: 11000.1042
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-351-348-74
Query Match 15.4%; Score 440; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 5.2e-31;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 284 DRQASRTVSGVPVSVNLVSGIRGRCRPTTTRAVAIATLASRGVVAPOAGDVAAAAAG 343
Db 1 DRQASRTVSGVPVSVNLVSGIRGRCRPTTTRAVAIATLASRGVVAPOAGDVAAAAAG 60
QY 344 SPWPVRSVARPVAVLRTGPPRRPSDT 370
Db 61 SPWPVRSVARPVAVLRTGPPRRPSDT 87
RESULT 11
US-09-450-072-70
; Sequence 70, Application US/09450072
```

```
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT FILING DATE: 1999-11-29
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-450-072-70
Query Match 13.6%; Score 389; DB 3; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IYSTPADRAYPGGLTYSGHPLATACAVATINAMEDGVMVANAARIGEQLGFLRDLAAR 60
Db 1 IYSTPADRAYPGGLTYSGHPLATACAVATINAMEDGVMVANAARIGEQLGFLRDLAAR 60
QY 61 HRSVGEVRGLGVFWA 75
Db 61 HRSVGEVRGLGVFWA 75
RESULT 12
US-09-351-348-70
; Sequence 70, Application US/09351348
; Patent No. 6436898
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; FILE REFERENCE: 11000.1042
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-351-348-70
Query Match 13.6%; Score 389; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IYSTPADRAYPGGLTYSGHPLATACAVATINAMEDGVMVANAARIGEQLGFLRDLAAR 60
Db 1 IYSTPADRAYPGGLTYSGHPLATACAVATINAMEDGVMVANAARIGEQLGFLRDLAAR 60
QY 61 HRSVGEVRGLGVFWA 75
Db 61 HRSVGEVRGLGVFWA 75
RESULT 13
US-09-450-072-69
; Sequence 69, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT FILING DATE: 1999-07-12
```

```
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 69
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-450-072-69

Query Match      13.0%; Score 373; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.7e-25;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 472 IAATGVPGTATVIRQYPKLLRAKANWEDTTFPSIEEKHRPRGSGVAGPVFRVNLGRAIP 531
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1 IAATGVPGTATVIRQYPKLLRAKANWEDTTFPSIEEKHRPRGSGVAGPVFRVNLGRAIP 60

Qy 532 SRAARAAEIH 541
    ||||||||
Db 61 SRAARAAEIH 70
```

```
RESULT 14
US-09-351-348-69
; Sequence 69, Application US/09351348
; Patent No. 6436898
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines
; FILE REFERENCE: 11000.1042
; CURRENT APPLICATION NUMBER: US/09/351,348
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 69
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-351-348-69

Query Match      13.0%; Score 373; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.7e-25;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 472 IAATGVPGTATVIRQYPKLLRAKANWEDTTFPSIEEKHRPRGSGVAGPVFRVNLGRAIP 531
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1 IAATGVPGTATVIRQYPKLLRAKANWEDTTFPSIEEKHRPRGSGVAGPVFRVNLGRAIP 60

Qy 532 SRAARAAEIH 541
    ||||||||
Db 61 SRAARAAEIH 70
```

```
RESULT 15
US-09-450-072-77
; Sequence 77, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; TITLE OF INVENTION: and Methods for their Use
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 59
```

```
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-450-072-77

Query Match      11.4%; Score 326; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e-21;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 DQLGEPGAQQORQGRGKHDRDRDVPAAQORPAVHPAGPGPADRVGVDPGRHRRARQGHQPRD 281
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1 DQLGEPGAQQORQGRGKHDRDRDVPAAQORPAVHPAGPGPADRVGVDPGRHRRARQGHQPRD 59

Db 1 DQLGEPGAQQORQGRGKHDRDRDVPAAQORPAVHPAGPGPADRVGVDPGRHRRARQGHQPRD 59

Search completed: September 16, 2005, 20:36:26
Job time : 27 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2005, 20:36:34 ; Search time 168 Seconds  
(without alignments)  
1263.878 Million cell updates/sec

Title: US-10-607-752-116  
Perfect score: 2862  
Sequence: 1 IYSTFADRAYPGGLTYSQHP.....IPSRARAEEIHGSHHHH 549

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2862	100.0	582	AAB31660	Aab31660 Amino aci
2	2145	74.9	582	AAB31659	Aab31659 Amino aci
3	1906	66.6	582	AAB31658	Aab31658 Amino aci
4	490	17.1	97	AAB31650	Aab31650 Amino aci
5	440	15.4	87	AAB31653	Aab31653 Amino aci
6	389	13.6	75	AAB31649	Aab31649 Amino aci
7	373	13.0	70	AAB31648	Aab31648 Amino aci
8	326	11.4	59	AAB31656	Aab31656 Amino aci
9	255	8.9	49	AAB31651	Aab31651 Amino aci
10	237	8.3	46	AAB31652	Aab31652 Amino aci
11	224	7.8	44	AAB31655	Aab31655 Amino aci
12	222	7.8	456	AAB31655	Aab31655 Amino aci
13	220	7.7	445	AAB31655	Aab31655 Amino aci
14	206	7.2	38	AAB31646	Aab31646 Amino aci
15	204.5	7.1	819	AAB31646	Aab31646 Amino aci
16	197.5	6.9	900	AAB31646	Aab31646 Amino aci
17	196.5	6.9	606	AAB31646	Aab31646 Amino aci
18	196	6.8	613	AAB31646	Aab31646 Amino aci
19	194	6.8	973	AAB31646	Aab31646 Amino aci
20	192	6.7	802	AAB31646	Aab31646 Amino aci
21	191.5	6.7	672	AAB31646	Aab31646 Amino aci
22	190.5	6.7	1037	AAB31646	Aab31646 Amino aci
23	190.5	6.7	618	AAB31646	Aab31646 Amino aci
24	190.5	6.7	957	AAB31646	Aab31646 Amino aci
25	189.5	6.6	588	AAB31646	Aab31646 Amino aci

26	188.5	6.6	19938	6	ABP76678	Abp76678 Streptomy
27	186	6.5	726	7	ABO71929	AbO71929 Pseudomon
28	185	6.5	1246	7	ABO74394	AbO74394 Pseudomon
29	184.5	6.4	1139	4	AAU30127	AAU30127 Novel hum
30	183	6.4	19938	6	ABP76682	Abp76682 Streptomy
31	180.5	6.3	412	7	ABO74447	AbO74447 Pseudomon
32	180.5	6.3	822	7	ABO73733	AbO73733 Pseudomon
33	180.5	6.3	1706	7	ABO83014	AbO83014 Pseudomon
34	180	6.3	410	4	AAU79786	AAU79786 Coryneb
35	180	6.3	410	4	AAU79799	AAU79799 Coryneb
36	180	6.3	410	4	AAU79893	AAU79893 Coryneb
37	180	6.3	410	4	AAU79636	AAU79636 Coryneb
38	180	6.3	410	4	AAU71868	AAU71868 C. glutam
39	180	6.3	438	4	AAU92427	AAU92427 C. glutam
40	180	6.3	456	4	AAU79892	AAU79892 Coryneb
41	180	6.3	456	4	AAU79635	AAU79635 Coryneb
42	180	6.3	456	4	AAU79785	AAU79785 Coryneb
43	180	6.3	456	4	AAU79798	AAU79798 Coryneb
44	180	6.3	456	4	AAU71867	AAU71867 C. glutam
45	180	6.3	456	7	ADD13563	ADD13563 C. glutam

ALIGNMENTS

RESULT 1  
AAB31660

ID AAB31660 standard; protein; 582 AA.

XX AC AAB31660;

XX DT 30-APR-2001 (first entry)

XX DE Amino acid sequence of an 8-mer multi-epitope designated ME/D.

XX KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
cancer; mycobacterial infection; TH1 immune response; vaccine.

XX OS Synthetic.

XX OS Mycobacterium vaccae.

XX PN WO200104140-A1.

XX PD 18-JAN-2001.

XX PF 10-JUL-2000; 2000WO-NZ000121.

XX PR 12-JUL-1999; 99US-00351348.

XX PR 29-NOV-1999; 99US-00450072.

XX (GENE-) GENESIS RES & DEV CORP. LTD.

XX PI Delcayre A;

XX DR WPI; 2001-168411/17.

XX XX N-PSDB; AAP25122.

XX PT Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
vaccae, useful for treating mycobacterial infections, immune disorders  
and cancers.

XX PS Claim 10; Page 75-76; 80pp; English.

XX CC The specification describes an immunogenic epitope of a Mycobacterium  
vaccae antigen. The epitope is a stimulator of cytokine production. The  
epitopes are useful for the treatment of immune disorders, infectious  
diseases, especially tuberculosis, and cancer. They are also useful for  
treatment of other mycobacterial infections such as those caused by  
Mycobacterium avium. The epitopes are especially useful for inducing TH1  
immune responses, and for producing vaccines. The present sequence  
represents an 8-mer multi-epitope designated ME/D

SQ Sequence 582 AA;

Query Match 100.0%; Score 2862; DB 4; Length 582;  
Best Local Similarity 100.0%; Pred. No. 8e-215;  
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTADRAYPGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60  
DB 34 IYSTADRAYPGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 93

QY 61 HRSVGEVRLGVFWAGSDPERAGLVEVLGAQCRDRDVGADAAAVGLGPGQRHARA 120  
DB 94 HRSVGEVRLGVFWAGSDPERAGLVEVLGAQCRDRDVGADAAAVGLGPGQRHARA 153

QY 121 DGSISALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
DB 154 DGSISALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 213

QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGASDQIGEPGAQQRQKHRD 240  
DB 214 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGASDQIGEPGAQQRQKHRD 273

QY 241 RRDVPAQQRPAVHPAGPGPADRVGDPGRRRARGQHOPRQSDRQASRTVSGVPVSNV 300  
DB 274 RRDVPAQQRPAVHPAGPGPADRVGDPGRRRARGQHOPRQSDRQASRTVSGVPVSNV 333

QY 301 LSAGIRCRTPPTTRAVAIATLASRGVVAPOPAGDVVARAAAAGSPWPVRSVARPVAVLRT 360  
DB 334 LSAGIRCRTPPTTRAVAIATLASRGVVAPOPAGDVVARAAAAGSPWPVRSVARPVAVLRT 393

QY 361 GPPRRPSDTGSIQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 420  
DB 394 GPPRRPSDTGSIQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 453

QY 421 IGSIALRCGKDEAVALHYVAPVGEKQDYIDRALRNI GPYLPALVGSIAATGPVPG 480  
DB 454 IGSIALRCGKDEAVALHYVAPVGEKQDYIDRALRNI GPYLPALVGSIAATGPVPG 513

QY 481 TAWIVROYPKLRAKANWEDTWTFFSIEKHPRGSGVGPVFRVNLGRAIPSAARAABE 540  
DB 514 TAWIVROYPKLRAKANWEDTWTFFSIEKHPRGSGVGPVFRVNLGRAIPSAARAABE 573

QY 541 HGSHHHHH 549  
DB 574 HGSHHHHH 582

RESULT 2  
AAB31659  
ID AAB31659 standard; protein; 582 AA.  
XX AAB31659;  
AC AAB31659;  
DT 30-APR-2001 (first entry)  
XX  
DE Amino acid sequence of an 8-mer multi-epitope designated ME/B.  
XX  
KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
KW cancer; mycobacterial infection; TH1 immune response; vaccine.  
XX  
OS Synthetic.  
OS Mycobacterium vaccae.  
XX  
XX WO200104140-A1.  
FN  
PD 18-JAN-2001.  
XX  
PF 10-JUL-2000; 2000WO-NZ000121.  
XX  
PR 12-JUL-1999; 99US-00351348.  
XX 29-NOV-1999; 99US-00450072.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX

PI Delcayre A;  
XX WPI; 2001-168411/17.  
DR N-PSDB; AAF25121.  
XX  
PT Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
PT vaccae, useful for treating mycobacterial infections, immune disorders  
PT and cancers.  
XX  
XX Claim 10; Page 74-75; 80pp; English.  
XX  
CC The specification describes an immunogenic epitope of a Mycobacterium  
CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
CC epitopes are useful for the treatment of immune disorders, infectious  
CC diseases, especially tuberculosis, and cancer. They are also useful for  
CC treatment of other mycobacterial infections such as those caused by  
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
CC immune responses, and for producing vaccines. The present sequence  
CC represents an 8-mer multi-epitope designated ME/B  
XX  
SQ Sequence 582 AA;  
Query Match 74.9%; Score 2145; DB 4; Length 582;  
Best Local Similarity 67.4%; Pred. No. 8.7e-159;  
Matches 442; Conservative 0; Mismatches 0; Indels 214; Gaps 4;

QY 1 IYSTADRAYPGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60  
DB 34 IYSTADRAYPGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 93

QY 61 HRSVGEVRLGVFWAGSDPERAGLVEVLGAQCRDRDVGADAAAVGLGPGQRHARA 120  
DB 94 HRSVGEVRLGVFWAGSDPERAGLVEVLGAQCRDRDVGADAAAVGLGPGQRHARA 108

QY 121 DGSISALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180  
DB 109 -GSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 167

QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGASDQIGEPGAQQRQKHRD 240  
DB 168 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGA----- 207

QY 241 RRDVPAQQRPAVHPAGPGPADRVGDPGRRRARGQHOPRQSDRQASRTVSGVPVSNV 300  
DB 208 -----GSDRQASRTVSGVPVSNV 226

QY 301 LSAGIRCRTPPTTRAVAIATLASRGVVAPOPAGDVVARAAAAGSPWPVRSVARPVAVLRT 360  
DB 227 LSAGIRCRTPPTTRAVAIATLASRGVVAPOPAGDVVARAAAAGSPWPVRSVARPVAVLRT 286

QY 361 GPPRRPSDT----- 370  
DB 287 GPPRRPSDTGSDQIGEPGAQQRQKHRDRDVPAAQRPVHPAGPGPADRVGDPGRH 346

QY 371 -----GSIQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGT 419  
DB 347 RRARGQHOPRQSDGSIQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGT 406

QY 420 EIGSIARLCGKDEAVALHYVAPVGEKQDYIDRALRNI GPYLPALVGSIAATGPVPG 469  
DB 407 EIGSIARLCGKDEAVALHYVAPVGEKQDYIDRALRNI GPYLPALVGSIAATGPVPG 466

QY 470 -----GSIATGVPVGTAWIVROYPKL 493  
DB 467 VEVLGAQCRDRDVGADAAAVGLGPGQRHARADGSIATGVPVGTAWIVROYPKL 526

QY 494 AKANWEDTWTFFSIEKHPRGSGVGPVFRVNLGRAIPSAARAABEIHGSHHHHH 549  
DB 527 AKANWEDTWTFFSIEKHPRGSGVGPVFRVNLGRAIPSAARAABEIHGSHHHHH 582

RESULT 3  
AAB31658

ID XX AAB31658 standard; protein; 582 AA.  
 AC AAB31658;  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Amino acid sequence of an 8-mer multi-epitope designated ME/A.  
 XX  
 KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
 KW cancer; mycobacterial infection; TH1 immune response; vaccine.  
 XX  
 OS Synthetic.  
 OS Mycobacterium vaccae.  
 XX  
 PN WO200104140-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 10-JUL-2000; 2000WO-NZ000121.  
 XX  
 PR 12-JUL-1999; 99US-00351348.  
 PR 29-NOV-1999; 99US-00450072.  
 XX  
 (GENE-) GENESIS RES & DEV CORP LTD.  
 XX  
 PI Delcayre A;  
 XX  
 DR WPI; 2001-168411/17.  
 DR N-PSDB; AAF25120.  
 XX  
 XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
 PT vaccae, useful for treating mycobacterial infections, immune disorders  
 PT and cancers.  
 XX  
 XX Claim 10; Page 73-74; 80pp; English.  
 XX  
 CC The specification describes an immunogenic epitope of a Mycobacterium  
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
 CC epitopes are useful for the treatment of immune disorders, infectious  
 CC diseases, especially tuberculosis, and cancer. They are also useful for  
 CC treatment of other mycobacterial infections such as those caused by  
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
 CC immune responses, and for producing vaccines. The present sequence  
 CC represents an 8-mer multi-epitope designated ME/A  
 XX  
 SQ Sequence 582 AA;  
 Query Match 66.6%; Score 1906; DB 4; Length 582;  
 Best Local Similarity 57.1%; Pred. No. 4.1e-140;  
 Matches 399; Conservative 0; Mismatches 0; Indels 300; Gaps 2;  
 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDGVMNAAIRIGEVLGFLDIAAR 60  
 34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDGVMNAAIRIGEVLGFLDIAAR 93  
 61 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGACRRDVVAGDAAAVGLGPGORHARA 120  
 94 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGACRRDVVAGDAAAVGLGPGORHARA 153  
 121 ----- 120  
 154 DGSQRQASRTSGVPVSNVLSAGIRCRTPTTTRAVAICLATLASRGVAPAGDVARAA 213  
 121 ----- 120  
 214 AAGSPWVRSVARPVAVLRTGPPRRPSDTGSDQLGEPGAQORQKHKRDREDVPAQORP 273  
 121 ----- DGSISLVAASPPRAASAPASIGLPGSGQ 150  
 274 AVHPAGPGPADRVGDPGHRERARQHQPRDGSISLVAASPPRAASAPASIGLPGSGQ 333  
 151 HTSIHPRSSNGSPVTHISQSMNAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQSAS 210  
 DB 334 HTSIHPRSSNGSPVTHISQSMNAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQSAS 393  
 QY 211 TCTDGNDSGAGSDQLGEPGAQORQKHKRDREDVPAQORPVAHPAGPGPADRVGDPGHR 270  
 DT TCTDGNDSGA----- 403  
 XX  
 DE 271 RRARQHQPRDGSQRQASRTSGVPVSNVLSAGIRCRTPTTTRAVAICLATLASRGVAP 330  
 XX  
 KW 404 ----- 403  
 XX  
 OS 331 QPAGDVARAAAGSPWVRSVARPVAVLRTGPPRRPSDTGSDITQVGRPAVLFAPEQR 390  
 OS -GSITQVGRPAVLFAPEQR 423  
 XX  
 PN 391 RRADORSRCRQHPGGGRHVQIVASARGTVEIGSIARLCGKDEAVAAALHVAVPVGKQDYI 450  
 XX  
 PD 424 RRADORSRCRQHPGGGRHVQIVASARGTVEIGSIARLCGKDEAVAAALHVAVPVGKQDYI 483  
 XX  
 PF 451 DRALRNIGPYLPAEVPALVGSIAATGPVPGTAWIVRQYPKLIIRAKANMEDTWTFFSIEBK 510  
 XX  
 PR 484 DRALRNIGPYLPAEVPALVGSIAATGPVPGTAWIVRQYPKLIIRAKANMEDTWTFFSIEBK 543  
 XX  
 (GENE-) GENESIS RES & DEV CORP LTD.  
 XX  
 PI Delcayre A;  
 XX  
 DR WPI; 2001-168411/17.  
 DR N-PSDB; AAF25081.  
 XX  
 XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
 PT vaccae, useful for treating mycobacterial infections, immune disorders  
 PT and cancers.  
 XX  
 XX Claim 1; Page 70-71; 80pp; English.  
 XX  
 CC The specification describes an immunogenic epitope of a Mycobacterium  
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
 CC epitopes are useful for the treatment of immune disorders, infectious  
 CC diseases, especially tuberculosis, and cancer. They are also useful for  
 CC treatment of other mycobacterial infections such as those caused by  
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
 CC immune responses, and for producing vaccines. The present sequence  
 CC represents a M. vaccae epitope of the invention  
 XX

SQ Sequence 97 AA; Query Match 17.1%; Score 490; DB 4; Length 97; Best Local Similarity 100.0%; Pred. No. 1.8e-30; Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 ISSALVASPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSNMAASSGTSRRSS 183  
DB 1 ISSALVASPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSNMAASSGTSRRSS 60

QY 184 TLFWRQSPCMIPGSASSGLRESSQSASTCTDGNDSGA 220  
DB 61 TLFWRQSPCMIPGSASSGLRESSQSASTCTDGNDSGA 97

RESULT 5  
331653  
AAB31653 standard; peptide; 87 AA.

AC AAB31653;  
DT 30-APR-2001 (first entry)  
DE Amino acid sequence of a M. vaccae immunogenic epitope from DNA37.  
XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
KW cancer; mycobacterial infection; TH1 immune response; vaccine.  
XX Mycobacterium vaccae.  
XX WO200104140-A1.  
XX 18-JAN-2001.  
XX 10-JUL-2000; 2000WO-NZ000121.  
XX 12-JUL-1999; 99US-00351348.  
XX 29-NOV-1999; 99US-00450072.  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX Delcayre A;  
XX WPI; 2001-168411/17.  
XX N-PSDB; AAF25084.  
XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium vaccae, useful for treating mycobacterial infections, immune disorders and cancers.  
XX Claim 1; Page 71; 80pp; English.

PS The specification describes an immunogenic epitope of a Mycobacterium vaccae antigen. The epitope is a stimulator of cytokine production. The epitopes are useful for the treatment of immune disorders, infectious diseases, especially tuberculosis, and cancer. They are also useful for treatment of other mycobacterial infections such as those caused by Mycobacterium avium. The epitopes are especially useful for inducing TH1 immune responses, and for producing vaccines. The present sequence represents a M. vaccae epitope of the invention

XX Query Match 15.4%; Score 440; DB 4; Length 87;  
PS Best Local Similarity 100.0%; Pred. No. 1.3e-26; Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 DRQASRTVSGVPVESNVLSAGICRTPPTTRAVAI CIATLASRGVAPQAGDVARAAAG 343  
DB 1 DRQASRTVSGVPVESNVLSAGICRTPPTTRAVAI CIATLASRGVAPQAGDVARAAAG 60

QY 344 SPWPVRSVARPVAVLRTGPPRRPST 370  
DB 1 SPWPVRSVARPVAVLRTGPPRRPST 87

RESULT 6  
AAB31649  
ID AAB31649 standard; peptide; 75 AA.  
XX AAB31649;  
AC AAB31649;  
DT 30-APR-2001 (first entry)  
DE Amino acid sequence of a M. vaccae immunogenic epitope from DNA9A.  
XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
KW cancer; mycobacterial infection; TH1 immune response; vaccine.  
XX Mycobacterium vaccae.  
XX WO200104140-A1.  
XX 18-JAN-2001.  
XX 10-JUL-2000; 2000WO-NZ000121.  
XX 12-JUL-1999; 99US-00351348.  
XX 29-NOV-1999; 99US-00450072.  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX Delcayre A;  
XX WPI; 2001-168411/17.  
XX N-PSDB; AAF25080.  
XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium vaccae, useful for treating mycobacterial infections, immune disorders and cancers.  
XX Claim 1; Page 70; 80pp; English.

PS The specification describes an immunogenic epitope of a Mycobacterium vaccae antigen. The epitope is a stimulator of cytokine production. The epitopes are useful for the treatment of immune disorders, infectious diseases, especially tuberculosis, and cancer. They are also useful for treatment of other mycobacterial infections such as those caused by Mycobacterium avium. The epitopes are especially useful for inducing TH1 immune responses, and for producing vaccines. The present sequence represents a M. vaccae epitope of the invention

XX Query Match 13.6%; Score 389; DB 4; Length 75;  
PS Best Local Similarity 100.0%; Pred. No. 1e-22; Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQVLGPGRLDLAAR 60  
DB 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQVLGPGRLDLAAR 60

QY 61 HRSVGEVRLGLGVFWA 75  
DB 61 HRSVGEVRLGLGVFWA 75

RESULT 7  
AAB31648  
ID AAB31648 standard; peptide; 70 AA.  
XX AAB31648;  
AC AAB31648;  
DT 30-APR-2001 (first entry)  
DE Amino acid sequence of a M. vaccae immunogenic epitope from DNA5.



CC The specification describes an immunogenic epitope of a Mycobacterium  
CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
CC epitopes are useful for the treatment of immune disorders, infectious  
CC diseases, especially tuberculosis, and cancer. They are also useful for  
CC treatment of other mycobacterial infections such as those caused by  
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
CC immune responses, and for producing vaccines. The present sequence  
CC represents a M. vaccae epitope of the invention  
XX  
SQ Sequence 49 AA;

Query Match 8.9%; Score 255; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.7e-12; Indels 0; Gaps 0;  
Matches 49; Conservative 0; Mismatches 0;

QY 373 ITQVGRPAVLFAPEQRCRRRQSCQRIHPGGRHVQIVASARGTVEI 421  
1 ITQVGRPAVLFAPEQRCRRRQSCQRIHPGGRHVQIVASARGTVEI 49

RESULT 10  
AAB31652  
ID AAB31652 standard; peptide; 46 AA.

AC AAB31652;

XX 30-APR-2001 (first entry)

XX Amino acid sequence of a M. vaccae immunogenic epitope from DNA29.

XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
XX cancer; mycobacterial infection; TH1 immune response; vaccine.

XX Mycobacterium vaccae.

XX WO200104140-A1.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-NZ000121.

XX 12-JUL-1999; 99US-00351348.

XX 29-NOV-1999; 99US-00450072.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Delcayre A;

XX WPI; 2001-168411/17.

XX N-PSDB; AAF25083.

XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
XX vaccae, useful for treating mycobacterial infections, immune disorders  
XX and cancers.

XX Claim 1; Page 71; 80pp; English.

XX The specification describes an immunogenic epitope of a Mycobacterium  
XX vaccae antigen. The epitope is a stimulator of cytokine production. The  
XX epitopes are useful for the treatment of immune disorders, infectious  
XX diseases, especially tuberculosis, and cancer. They are also useful for  
XX treatment of other mycobacterial infections such as those caused by  
XX Mycobacterium avium. The epitopes are especially useful for inducing TH1  
XX immune responses, and for producing vaccines. The present sequence  
XX represents a M. vaccae epitope of the invention  
XX

SQ Sequence 46 AA;

Query Match 8.3%; Score 237; DB 4; Length 46;  
Best Local Similarity 100.0%; Pred. No. 4.1e-11; Indels 0; Gaps 0;  
Matches 46; Conservative 0; Mismatches 0;

QY 424 IARLCGKDEAVALHYVAPVGEKQDYIDRALRNIGPILPAEVPAIV 469

Db 1 IARLCGKDEAVALHYVAPVGEKQDYIDRALRNIGPILPAEVPAIV 46

RESULT 11

AAB31655  
ID AAB31655 standard; peptide; 44 AA.

AC AAB31655;

XX 30-APR-2001 (first entry)

XX Amino acid sequence of a M. vaccae immunogenic epitope from DNA44.

XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
XX cancer; mycobacterial infection; TH1 immune response; vaccine.

XX Mycobacterium vaccae.

XX WO200104140-A1.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-NZ000121.

XX 12-JUL-1999; 99US-00351348.

XX 29-NOV-1999; 99US-00450072.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Delcayre A;

XX WPI; 2001-168411/17.

XX N-PSDB; AAF25086.

XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
XX vaccae, useful for treating mycobacterial infections, immune disorders  
XX and cancers.

XX Claim 1; Page 72; 80pp; English.

XX The specification describes an immunogenic epitope of a Mycobacterium  
XX vaccae antigen. The epitope is a stimulator of cytokine production. The  
XX epitopes are useful for the treatment of immune disorders, infectious  
XX diseases, especially tuberculosis, and cancer. They are also useful for  
XX treatment of other mycobacterial infections such as those caused by  
XX Mycobacterium avium. The epitopes are especially useful for inducing TH1  
XX immune responses, and for producing vaccines. The present sequence  
XX represents a M. vaccae epitope of the invention  
XX

SQ Sequence 44 AA;

Query Match 7.8%; Score 224; DB 4; Length 44;  
Best Local Similarity 100.0%; Pred. No. 4e-10; Indels 0; Gaps 0;  
Matches 44; Conservative 0; Mismatches 0;

QY 78 DPERAGLRVEVLGAQCRRRDVVAGDAAAVGLGFPQQRHARAD 121  
1 DPERAGLRVEVLGAQCRRRDVVAGDAAAVGLGFPQQRHARAD 44

RESULT 12

ABO66648  
ID ABO66648 standard; protein; 456 AA.

AC ABO66648;

XX 29-JUL-2004 (first entry)

XX Klebsiella pneumoniae polypeptide seqid 13165.

XX Recombinant expression vector; transcription regulatory element;  
XX Klebsiella pneumoniae protein; antibacterial; Vaccine.

XX Klebsiella pneumoniae.  
 XX US6610836-B1.  
 XX 26-AUG-2003.  
 XX 27-JAN-2000; 2000US-00489039.  
 XX 29-JAN-1999; 99US-0117747P.  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 XX Breton GL, Osborne M;  
 PI WPI; 2003-895346/82.  
 DR N-PSDB; ABD00219.  
 XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
 PT preparing a vaccine composition against Klebsiella pneumoniae.  
 XX Disclosure; SEQ ID NO 13165; 932pp; English.  
 PS The invention describes a new isolated nucleic acid encoding a Klebsiella  
 CC pneumoniae polypeptide. Also described are: a recombinant expression  
 CC vector comprising the nucleic acid, operably linked to a transcription  
 CC regulatory element; and a cell comprising the recombinant expression  
 CC vector. The nucleic acid is useful for preparing a vaccine composition  
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
 CC Klebsiella pneumoniae polypeptide of the invention  
 XX Sequence 456 AA;  
 SQ

Query Match 7.8%; Score 222; DB 7; Length 456;  
 Best Local Similarity 46.2%; Pred. No. 1.2e-08;  
 Matches 49; Conservative 17; Mismatches 30; Indels 10; Gaps 1;  
 QY 5 FADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQVLGPGRLDAAARHSV 64  
 DB 315 FDDHFFAGGLTYSGHPLAIAVAITIDAMKEENVVNAASIGNEVLRPGLEALAEKHAI 374  
 QY 65 GEVRGLGVFWAGSDPERAGLVEVLGAQCRRRDVVVGAGDAAAVGV 110  
 DB 375 GEVRGRLGFOA-----LELVSSREQTKPLTAADMAAATKGA 410

RESULT 13  
 AAU36108  
 ID AAU36108 standard; protein; 445 AA.  
 XX AAU36108;  
 DT 14-FEB-2002 (first entry)  
 XX Klebsiella pneumoniae cellular proliferation protein #96.  
 XX Antisense; prokaryotic cellular proliferation protein; antibiotic;  
 KW antibacterial; drug design.  
 XX Klebsiella pneumoniae.  
 OS WO200170955-A2.  
 XX 27-SEP-2001.  
 XX 21-MAR-2001; 2001WO-US009180.  
 XX 21-MAR-2000; 2000US-0191078P.  
 XX 23-MAY-2000; 2000US-0208648P.  
 XX 26-MAY-2000; 2000US-0207727P.  
 XX 23-OCT-2000; 2000US-0242578P.  
 XX 27-NOV-2000; 2000US-0253625P.  
 XX 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.  
 XX (ELIT-) ELITRA PHARM INC.  
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
 PI Yamamoto RT, Xu HH;  
 XX WPI; 2001-611495/70.  
 DR N-PSDB; AAS53967.  
 XX New polynucleotides for the identification and development of  
 PT antibiotics, comprise sequences of antisense nucleic acids.  
 XX Example 3; SEQ ID NO 11701; 511pp; English.  
 XX The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the genes,  
 CC their use in the discovery of novel antibiotics, the essential genes  
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
 CC useful for the identification of potential new targets for antibiotic  
 CC development. The antisense nucleic acids can also be used to identify  
 CC proteins used in proliferation, to express these proteins, and to obtain  
 CC antibodies capable of binding to the expressed proteins. The proteins can  
 CC be used to screen compounds in rational drug discovery programmes. The  
 CC antisense nucleic acid sequence is also useful to screen for homologous  
 CC nucleic acids which are required for cell proliferation in a wide variety  
 CC of organisms. The present sequence represents an essential prokaryotic  
 CC cellular proliferation protein. Note: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 445 AA;  
 SQ

Query Match 7.7%; Score 220; DB 4; Length 445;  
 Best Local Similarity 46.2%; Pred. No. 1.7e-08;  
 Matches 49; Conservative 17; Mismatches 30; Indels 10; Gaps 1;  
 QY 5 FADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQVLGPGRLDAAARHSV 64  
 DB 304 FDDHFFAGGLTYSGHPLAIAVAITIDAMKEENVVNAASIGNEVLRPGLEALAEKHAI 363  
 QY 65 GEVRGLGVFWAGSDPERAGLVEVLGAQCRRRDVVVGAGDAAAVGV 110  
 DB 364 GEVRGRLGFOA-----LELVSSREQTKPLTAADMAAATKGA 399

RESULT 14  
 AAB31646  
 ID AAB31646 standard; peptide; 38 AA.  
 XX AAB31646;  
 AC AAB31646;  
 XX 30-APR-2001 (first entry)  
 XX Amino acid sequence of a M. vaccae immunogenic epitope from DNA27.  
 DE Epitope; antigen; cytokine production; immune disorder; tuberculosis;  
 KW cancer; mycobacterial infection; TH1 immune response; vaccine.  
 XX Mycobacterium vaccae.  
 OS WO200104140-A1.  
 XX 18-JAN-2001.  
 XX 10-JUL-2000; 2000WO-NZ000121.  
 XX 12-JUL-1999; 99US-00351348.  
 XX 29-NOV-1999; 99US-00450072.

PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX Delcayre A;  
XX WPI; 2001-168411/17.  
DR N-PSDB; AAF25077.  
XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium  
PT vaccae, useful for treating mycobacterial infections, immune disorders  
PT and cancers.  
XX Claim 1; Page 70; 80pp; English.  
XX The specification describes an immunogenic epitope of a Mycobacterium  
CC vaccae antigen. The epitope is a stimulator of cytokine production. The  
CC epitopes are useful for the treatment of immune disorders, infectious  
CC diseases, especially tuberculosis, and cancer. They are also useful for  
CC treatment of other mycobacterial infections such as those caused by  
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1  
CC immune responses, and for producing vaccines. The present sequence  
CC represents a M. vaccae epitope of the invention  
XX Sequence 38 AA;  
SQ  
Query Match 7.2%; Score 206; DB 4; Length 38;  
Best Local Similarity 100.0%; Pred. No. 8.4e-09; Mismatches 0; Indels 0; Gaps 0;  
Matches 38; Conservative 0;  
QY 373 ITQVGRPAVLFAPEQRCRRRDRQSCRIHPGGRHVQ 410  
DB 1 ITQVGRPAVLFAPEQRCRRRDRQSCRIHPGGRHVQ 38  
RESULT 15  
ABO70823  
ID ABO70823 standard; protein; 819 AA.  
XX ABO70823;  
XX ABO70823;  
XX 29-JUL-2004 (first entry)  
XX Pseudomonas aeruginosa polypeptide #2998.  
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX Pseudomonas aeruginosa.  
PN US6551795-B1.  
XX 22-APR-2003.  
XX 18-FEB-1999; 99US-00252991.  
XX 18-FEB-1998; 98US-0074788P.  
XX 27-JUL-1998; 98US-0094190P.  
XX (GENO-) GENOME THERAPEUTICS CORP.  
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX WPI; 2003-615309/58.  
XX N-PSDB; ABD04394.  
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, of  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX Disclosure; SEQ ID NO 19569; 455pp; English.  
XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a

CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 819 AA;  
Query Match 7.1%; Score 204.5; DB 7; Length 819;  
Best Local Similarity 25.5%; Pred. No. 6.1e-07;  
Matches 161; Conservative 53; Mismatches 241; Indels 177; Gaps 34;  
QY 9 AYPG--GLTYSGHPLATACAVATTNAMEDGVMANARIGEOVLGPGLRDLAARRHSVGE 66  
DB 202 AFGNVGALVRGCDGHARAAAVMHGQQPGGLASRSVGAG----GSGQRDPAGDPG-DQ 256  
QY 67 VRGLGVFWAGSDPERAGLRVEVLGACQCRRRDVVGAGDAAAVGVGLGPOR-OHRA----- 118  
DB 257 LRG-----PDAPALRLHL-----RAPAAAGRRHQHVRHRADELPEHL 295  
QY 119 ---RAD--GSTSSALVASPPRAASAPASIGLGPS-----GQHTSIHPRSSNGSPVTHI 167  
DB 296 FHRADRRPRVPRVPAAFRAAAVPAAD-GLDPHSLRPLGLGDHGAQPPRAASG----- 348  
QY 168 SQSNAAASSGTSRRSSSTLFRWQSPCMIPGSSGLRESSQSASTC--TDGNDSSAGSDQL 225  
DB 349 ---CHRRGAVPRRHGILGDRHGFVAGAAVQCGAVPDPARLFRRTPGRAVVPGDHLC 404  
QY 226 GEPGAQQRQKGRDRDVPQAQRPVHPAGPG-PADRVGVDPCGRHRRARQHOHPRDGS 284  
DB 405 GRPGTGPRPGAR-----PARRAYQLLPDGEALPA-----PGR-RNLLGAHQEVAGAR 450  
QY 285 ROASRTV----SGVPVESNVLISAGIRC--RT-----PTTRAVAILCLATL 322  
DB 451 RGGSRPVLRHFGGCVYQSQACRAGARPRRTDQAGHRRRRADRLHGLGVGPAQPPALGFPHV 510  
QY 323 A-----SRGVVAPOPA--GDVARAAAGSPWVRVSVARVPVAVLRTGPPRRPSD 369  
DB 511 RPVRHPORSRGRRGAVEGEPACGRSPRAARAGAR-----RORVAEIRLVRVPRPQP 564  
QY 370 TGSITQVGRPAVLFAPEQRCRR-----RADQRCRQIHPPGGRHVQIIVASARGTVEI 421  
DB 565 RGSPPAGDRHA-----DAERGQPSGADDRHQHRRHDPHGGN-----PARGKGTAG 612  
QY 422 GSI-ARLCGKD---EAVAALHYVAPVGEKQYIIRALRN----- 456  
DB 613 DPFVHRRCRVDHRRRRPRDLH--BFGGDDRLDLAGHRRHAPRTGLQARQRHRRGPGK 670  
QY 457 IGPVLPAREVPALV--GSTAATGPVGTAWIVRQYPKLLRAKAN--WEDTWTFFPSTEEXHR 512  
DB 671 PEAATLPAEHGVLPGGRRHADQPOGRAA----RIPELRCAGAHPRWRDHRHRAVGPERHQ 726  
QY 513 PRGSVAGVFRVNLGR--AIFPSRAARAETHG 542  
DB 727 GPGDAA---RAELSRPLCRCPHRAVQPHQVRG 754

Search completed: September 16, 2005, 20:55:01  
Job time : 171 secs